

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:59:57 ; search time 39 Seconds  
(without alignments)  
61.625 Million cell updates/sec

Title: US-09-549-642-20  
Perfect score: 138  
Sequence: 1 IVGXXEVTPHAYPMQVGLFIDDMYF 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73;\*: 1: pr1;\*: 2: pr2;\*: 3: pr3;\*: 4: pr4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	101	73.2	271	2	S29239	chymotrypsin (EC 3.4.21.1)
2	94	68.1	265	2	T10495	chymotrypsin (EC 3.4.21.1)
3	91	65.9	31	2	S61558	chymotrypsin Pm1
4	89	64.5	226	1	KCUF	brachyurin (EC 3.4.21.1)
5	80	58.0	31	1	S18356	chymotrypsin (EC 3.4.21.1)
6	74	53.6	309	2	B49878	coagulation factor
7	71	51.4	20	2	A56300	chymotrypsin I (EC 3.4.21.1)
8	69	50.0	271	1	A25528	pancreatic elastase
9	69	50.0	460	2	B61545	plasmin (EC 3.4.21.1)
10	69	50.0	1524	2	T30337	polyprotein - Afri
11	68	49.3	25	2	A23698	tryptase (EC 3.4.21.1)
12	67	48.6	23	2	P0036	serine proteinase
13	67	48.6	244	2	S72219	chymotrypsin B - A
14	67	48.6	268	2	S68826	pancreatic elastase
15	67	48.6	268	2	S68825	pancreatic elastase
16	66	47.8	271	1	ELR12	pancreatic elastase
17	65	47.1	262	1	A31372	granzyme A (EC 3.4.21.1)
18	64	46.4	269	2	B26523	pancreatic elastase
19	63	45.7	20	2	A34817	collagenolytic pro
20	63	45.7	269	1	A26823	pancreatic elastase
21	63	45.7	273	2	A41246	tryptase (EC 3.4.21.1)
22	63	45.7	274	2	A45754	tryptase (EC 3.4.21.1)
23	63	45.7	275	2	C35663	tryptase (EC 3.4.21.1)
24	63	45.7	812	1	PLMS	plasmin (EC 3.4.21.1)
25	63	45.7	812	1	PLBO	plasmin (EC 3.4.21.1)
26	63	45.7	1420	1	A32669	apolipropeptide (EC 3.4.21.1)
27	63	45.7	4548	1	S00557	apo-proteinase (EC 3.4.21.1)
28	62	44.9	24	2	PN0657	alkaline trypsin-1
29	62	44.9	331	2	T27906	hypothetical prote

## ALIGNMENTS

RESULT 1  
S29239  
chymotrypsin (EC 3.4.21.1) 1 precursor - penaeid shrimp (Penaeus vannamei)  
C:Species: Penaeus vannamei  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 22-Jun-1999  
C:Accession: S29239; S22075  
R:Sellios, D.; van Wormhoudt, A.  
FEBS Lett. 309, 219-224, 1992  
A:Title: Molecular cloning of a cDNA that encodes a serine protease with chymotryptic activity  
A:Reference number: S29239; MULID: 92387359; PMID: 1516690  
A:Molecule type: mRNA  
A:Residues: 1-271 <SEL>  
A:Cross reference: EMBL:X66415; PID:g10088; PID:g10089  
A:Note: the authors did not translate the codon for residue 1  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase  
E:16-271/Product: chymotrypsin 1 #status predicted <SIG>  
F:46-253/Domain: trypsin homology <TRY>  
F:86,132,223/Active site: His, Asp, Ser #status predicted

Query Match 73.2%; Score 101; DB 2; Length 271;  
Best Local Similarity 72.0%; Pred. No. 7.4e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
Db 46 IVGGVEATPHSNWQAAFLIDDMYF 70

RESULT 2  
T10495  
chymotrypsin (EC 3.4.21.1) BII - penaeid shrimp (Penaeus vannamei) (fragment)  
C:Species: Penaeus vannamei  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Jun-2000  
C:Accession: T10495  
R:Sellios, D.Y.; van Wormhoudt, A.  
submitted to the EMBL Data Library, January 1997  
A:Description: Polymorphism of chymotrypsin gene sequences in the shrimp.  
A:Reference number: Z17057  
A:Accession: T10495  
A:Status: translated from GB/EMBL/DDJB  
A:Molecule type: DNA  
A:Residues: 1-265 <SEL>  
C:Genetics:  
A:Note: chymotrypsin B  
A:Note: Intron positions not resolved (incomplete sequence)  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 68.1%; Score 94; DB 2; Length 265;  
 Best Local Similarity 68.0%; Pred. No. 8.6e-07;  
 Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 IVGGXEVTPHAYPWOVGLFIDDMYF 25

RESULT 3  
 S61538 chymotrypsin Pm1 - Penaeid shrimp (Penaeus monodon) (fragment)  
 C;Species: Penaeus monodon  
 C;Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 16-Feb-1997  
 C;Accession: SC1558 R;Tsai, I.H.; Lu, P.J.; Chuang, J.L.  
 Biochim. Biophys. Acta 1080, 59-67, 1991  
 A;Title: The midgut chymotrypsins of shrimps (Penaeus monodon, Penaeus japonicus and Penaeus japonicus) from the midgut of the shrimp Penaeus japonicus and Penaeus japonicus  
 A;Reference number: S18356; MUID:92031652; PMID:1657178  
 A;Accession: SC1558  
 Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-31 <TSA>  
 C;Superfamily: trypsin; trypsin homology  
 C;Keywords: protein digestion

Query Match 65.9%; Score 91; DB 2; Length 31;  
 Best Local Similarity 64.0%; Pred. No. 2.2e-07;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWOVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPWOVGLFIDDMYF 25

RESULT 4  
 KCUF brachyurin (EC 3.4.21.32) [validated] - Atlantic sand fiddler crab  
 N;Alternate names: collagenolytic proteinase U  
 C;Species: Uca pugillator (Atlantic sand fiddler crab)  
 C;Accession: A00958 C;Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 15-Sep-2000  
 R;Grant, G.A.; Henderson, K.O.; Eisen, A.Z.; Bradshaw, R.A.  
 A;Title: Amino acid sequence of a collagenolytic protease from the hepatopancreas of the  
 A;Accession number: A00958; MUID:81040004; PMID:6252953  
 A;Molecule type: protein  
 A;Residues: 1-226 <GRA>  
 A;Experimental source: tissue hepatopancreas  
 R;Perona, J.J.; Fletterick, R.J.  
 Submitted to the Brookhaven Protein Data Bank, November 1997  
 A;Reference number: A73134; PDB:1MZ  
 A;Contents: annotation; X-ray crystallography, 2.3 angstroms, residues 1-90, 'I', 92-146,  
 R;Perona, J.J.; Tsu, C.A.; Craik, C.S.; Fletterick, R.J.  
 Biochemistry 19, 4653-4659, 1980  
 A;Title: Crystal structure of an ecotin-collagenase complex suggests a model for recogni  
 A;Accession number: A59231; MUID:9729971; PMID:9154920  
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms  
 C;Complex: homodimer  
 C;Function:  
 C;Superfamily: trypsin; trypsin homology  
 C;Keywords: homodimer; hydrolase; protein degradation; protein digestion; serine protein  
 F;1-218/Domain: trypsin homology <TRY>  
 F;26-42 151-164,174-200/Disulfide bonds: #status experimental  
 F;41,87,178/Active site: His, Asp, Ser #status predicted

Query Match 64.5%; Score 89; DB 1; Length 226;  
 Best Local Similarity 64.0%; Pred. No. 4.2e-06;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWOVGLFIDDMYF 25

A: Note: a second variant, designated chymotrypsin II, had an identical N-terminal sequence  
 C: Comment: This enzyme has chymotryptic and collagenolytic activities.  
 C: Superfamily: trypsin; trypsin homology  
 C: Keywords: hydrolase; protein digestion; serine protease

Query Match Score 71; DB 2; Length 20;  
 Best Local Similarity 65.0%; Pred. No. 0.00016;  
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 Qy 1 IVGGXEVTHAYPHQVGFL 20  
 Db 1 IVGGXEVTHAYPHQVGFL 20

## RESULT 8

A25228 pancreatic elastase II (EC 3.4.21.71) precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 22-Jun-1999  
 C:Accession: A25228  
 C:Author: Stevenson, B.J.; Haganbuechle, O.; Wellauer, P.K.  
 C:Title: Sequence organisation and transcriptional regulation of the mouse elastase II  
 A:Reference number: A93646; MUID:87066713; PMID:3641189

A:Molecule type: mRNA  
 A:Residues: 1-271 <STEP>  
 A:Cross-references: GB:X04573; NID:950825; PIDN:CAA2242.1; PMID:950826  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine protease  
 F:1-30/#Domain: signal sequence #status predicted <SIG>  
 F:31-271/#Product: pancreatic elastase II #status predicted <MAT>  
 F:31-264/#Domain: trypsin homology <TRI>  
 F:75,123-218/Active site: His, Asp, Ser #status predicted  
 Query Match Score 50.0%; Pred. No. 0.006;  
 Best Local Similarity 61.1%; Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 IVGGXEVTHAYPHQVGFL 18  
 Db 31 VVGGQEATPTWPHQVSL 48

## RESULT 9

B61545 plasmin (EC 3.4.21.7) precursor - sheep (fragments)  
 N:Alternate names: plasminogen  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 28-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 17-Mar-1999  
 C:Accession: B61545; S8200  
 R:Schaller, J.; Rickli, E.E.  
 Enzyme 40, 63-69, 1988  
 A:Title: Structural aspects of the plasminogen of various species.  
 A:Reference number: A61545; MUID:89005015; PMID:3168975  
 A:Accession: B61545  
 A:Molecule type: protein  
 A:Residues: 1-37;38-117 <SCH>  
 R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.  
 Protein Seq. Data Anal. 5, 21-25, 1992  
 A:Title: Complete amino acid sequence of ovine miniplasminogen.  
 A:Reference number: S28200; MUID:93149995; PMID:1492292  
 A:Accession: S28200  
 A:Molecule type: protein  
 A:Residues: 118-460 <SCB>

C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine protease; z  
 F:1-37;38-117;118-460/Product: plasminogen (fragments) #status experimental <PRO>  
 F:1-37;38-117;118-460/Activation peptide (fragment) #status experimental <APT>  
 F:38-117;118-30;231-460/Product: plasmin (fragments) #status experimental <MAT>  
 F:41-118/#Domain: kringle homology <KRA>  
 F:118-460/Product: miniplasminogen #status experimental <MIN>

F;132-211/#Domain: kringle homology <KR5>  
 F;226-466/#Domain: plasmin chain B #status experimental <BCR>  
 F;272,315,410/Active site: His, Asp, Ser #status predicted

Query Match Score 69; DB 2; Length 460;  
 Best Local Similarity 61.1%; Pred. No. 0.011;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 IVGGXEVTHAYPHQVGFL 18  
 Db 231 VVGGCVATPHSWPMQVSL 248

## RESULT 10

A25228 polypeptidase - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
 C:Accession: T30337  
 R:Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.  
 submitted to the EMBL Data Library, March 1998  
 A:Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from  
 A:Reference number: A93646; MUID:87066713; PMID:3641189  
 A:Accession: T30337  
 A:Status: preliminary; translated from GB/EMBL/DDJB  
 A:Molecule type: mRNA  
 A:Residues: 1-1524 <YAN>  
 A:Cross-references: EMBL:U81290; NID:92981640; PMID:92981641; PIDN: AAC24717.1

Query Match Score 69; DB 2; Length 1524;  
 Best Local Similarity 57.9%; Pred. No. 0.042;  
 Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 IVGGXEVTHAYPHQVGFL 19  
 Db 584 IVGGGEASPNSPWMQVQIF 602

## RESULT 11

A23698 trypsin (EC 3.4.21.59), skin - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 31-Oct-1997  
 C:Accession: A23698  
 R:Braganza, V.J.; Simmons, W.H.  
 Biochemistry 30, 4997-5007, 1991  
 A:Title: Tryptase from rat skin: purification and properties.  
 A:Reference number: A23698; MUID:91242400; PMID:2036367  
 A:Accession: A23698  
 A:Molecule type: protein  
 A:Residues: 1-25 <BR>  
 C:Superfamily: trypsin; trypsin homology  
 C:Keywords: hydrolase; serine proteinase

Query Match Score 68; DB 2; Length 25;  
 Best Local Similarity 48.0%; Pred. No. 0.00058;  
 Matches 12; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 IVGGXEVTHAYPHQVGFLDDMF 25  
 Db 1 IVGGQEASGNKWPQVSLRYXDTW 25

## RESULT 12

P0036 serine proteinase (EC 3.4.21.-) - bovine (fragment)  
 N:Alternate names: trypsin-like proteinase bPTLP  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 22-Apr-1995  
 C:Accession: P0036; PU0039  
 R:Tsuiji, A.; Sakiyama, K.; Edazawa, K.; Nagata, K.; Nagamune, H.; Matsuda submitted to JIPID, September 1994

A; Description: Purification and characterization of a novel serine proteinase from bovine trypsin B

A; Reference number: PU0036

A; Molecule type: Protein

A; Accession: PU0036

A; Residues: 1-23 <TRSL>

A; Experimental source: Pancreas

C; Superfamily: trypsin; trypsin homology

C; Keywords: Hydrolase; serine proteinase

Query Match 48.6%; Score 67; DB 2; Length 23;

Best Local Similarity 50.0%; Pred. No. 0.00075;

Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGL 18

Db 1 VVGGEDAIFHHSWPWQISL 18

#### RESULT 13

**[REDACTED]** trypsin B - Atlantic cod (fragments)

C; Species: Gadus morhua (Atlantic cod)

C; Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Aug-1998

C; Accession: S72219

R; Ieth-Larsen, R.; Asgeirsson, B.; Thorolfsson, M.; Norregaard-Madsen, M.; Hojrup, P.

A; Title: Structure of chymotrypsin variant B from Atlantic cod, *Gadus morhua*.

A; Reference number: S72219; MUID:96439045; PMID:8841380

A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-14; 244 <LET>

C; Superfamily: trypsin; trypsin homology <TRY>

Query Match 48.6%; Score 67; DB 2; Length 244;

Best Local Similarity 61.1%; Pred. No. 0.011;

Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGL 18

Db 15 IVNGEAVPHHSWPWQVSL 32

#### RESULT 14

**[REDACTED]** pancreatic elastase (EC 3.4.21.36) isoform 2 precursor - human

C; Alternate names: caldebrin isoform 2

C; Species: Homo sapiens (man)

C; Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998

C; Accession: S68825

R; Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T.

F; FEBS Lett. 386, 26-28, 1996

A; Title: Molecular cloning and expression of human caldebrin.

A; Reference number: S68825; MUID:96221265; PMID:8635596

A; Molecule type: mRNA

A; Residues: 1-268 <TO>

A; Experimental source: pancreas

C; Superfamily: trypsin; trypsin homology

C; Keywords: hydrolase; pancreas; serine proteinase; zymogen

F; 1-16/Domain: signal sequence #status predicted <SIG>

F; 17-29/Domain: propeptide #status predicted <PRO>

F; 30-262/Domain: propeptide #status predicted <TRY>

Query Match 48.6%; Score 67; DB 2; Length 268;

Best Local Similarity 50.0%; Pred. No. 0.012;

Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGL 18

Db 30 VVGGEDAIFHHSWPWQISL 47

#### RESULT 15

**[REDACTED]** pancreatic elastase (EC 3.4.21.36) isoform 1 precursor - human

C; Alternate names: caldebrin isoform 1

C; Species: Homo sapiens (man)

C; Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 28-May-1999

C; Accession: S68825

R; Tomomura, A.; Akiyama, M.; Itoh, H.; Yoshino, I.; Tomomura, M.; Nishii, Y.; Noikura, T.

F; FEBS Lett. 386, 26-28, 1996

A; Title: Molecular cloning and expression of human caldebrin.

A; Reference number: S68825; MUID:96221265; PMID:8635596

A; Molecule type: mRNA

A; Residues: 1-268 <TO>

A; Experimental source: pancreas

C; Superfamily: trypsin; trypsin homology

C; Keywords: hydrolase; pancreas; serine proteinase; zymogen

F; 1-16/Domain: signal sequence #status predicted <SIG>

F; 17-29/Domain: propeptide #status predicted <PRO>

F; 30-262/Domain: propeptide #status predicted <TRY>

Query Match 48.6%; Score 67; DB 2; Length 268;

Best Local Similarity 50.0%; Pred. No. 0.012;

Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IVGGXEVTHAYPHQVGL 18

Db 30 VVGGEDAIFHHSWPWQISL 47

Result No.	Score	Query Match	Length	DB ID	Description
1	136	98.6	25	5 US-09-303-375A-1	Sequence 1, Appli
2	136	98.6	25	5 US-09-303-375A-2	Sequence 2, Appli
3	136	98.6	25	5 US-09-349-642-1	Sequence 1, Appli
4	136	98.6	25	5 US-09-549-642-2	Sequence 2, Appli
5	136	98.6	25	5 US-09-549-642-20	Sequence 20, Appli
6	136	98.6	300	5 US-09-644-022A-1	Sequence 1, Appli
7	101	73.2	25	5 US-09-644-022A-2	Sequence 2, Appli
8	101	73.2	25	5 US-09-503-375A-3	Sequence 3, Appli
9	101	73.2	25	5 US-09-549-642-3	Sequence 3, Appli
10	91	65.9	25	5 US-09-644-022A-6	Sequence 6, Appli
11	91	65.9	25	5 US-09-503-375A-7	Sequence 7, Appli
12	91	65.9	25	5 US-09-549-642-7	Sequence 7, Appli
13	89	64.5	25	5 US-09-644-022A-7	Sequence 8, Appli
14	89	64.5	25	5 US-09-503-375A-8	Sequence 8, Appli
15	89	64.5	25	5 US-09-549-642-8	Sequence 5, Appli
16	80	58.0	25	5 US-09-644-022A-5	Sequence 6, Appli
17	80	58.0	25	5 US-09-503-375A-6	Sequence 6, Appli
18	80	58.0	25	5 US-09-549-642-6	Sequence 6, Appli
19	75.5	54.7	287	1 PCT-US02-10780-110	Sequence 130, App
20	75.5	54.7	287	6 US-10-112-210	Sequence 130, App
21	75.5	54.7	602	7 US-60-452-610-23138	Sequence 23138, A
22	75.5	54.7	922	1 PCT-US02-10366-52	Sequence 52, Appli
23	75.5	54.7	932	6 US-10-163-937-6	Sequence 6, Appli
24	75.5	54.7	986	1 PCT-US02-10466-50	Sequence 50, Appli
25	70	50.7	273	6 US-10-219-051B-8824	Sequence 8824, Ap
26	70	50.7	273	6 US-10-219-051B-13255	Sequence 13255, A

NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 2  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-303-375A-2

Query Match 98.6%; Score 136; DB 5; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 SEQ ID NO 2  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-549-642-2

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RESULT 3  
 Sequence 1 Application US/09549642  
 GENERAL INFORMATION:  
 APPLICANT: Phairson Medical, Inc.  
 APPLICANT: de Faire, Johan  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Lindblom, Ragnvald  
 TITLE OF INVENTION: Removing Dental Plaque with Krill  
 FILE REFERENCE: 314572-101F  
 CURRENT APPLICATION NUMBER: US/09/549,642  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 09/303,375  
 PRIOR FILING DATE: 2000-04-30  
 PRIOR APPLICATION NUMBER: 08/600,273  
 PRIOR FILING DATE: 1996-02-08  
 PRIOR APPLICATION NUMBER: 08/486,820  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/385,540  
 PRIOR FILING DATE: 1995-02-08  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-549-642-1

Query Match 98.6%; Score 136; DB 5; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 SEQ ID NO 2  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-549-642-20

---

RESULT 5  
 Sequence 20 Application US/09549642  
 GENERAL INFORMATION:  
 APPLICANT: Phairson Medical, Inc.  
 APPLICANT: de Faire, Johan  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Kay, John  
 APPLICANT: Lindblom, Ragnvald  
 TITLE OF INVENTION: Removing Dental Plaque with Krill  
 FILE REFERENCE: 314572-101F  
 CURRENT APPLICATION NUMBER: US/09/549,642  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 09/303,375  
 PRIOR FILING DATE: 2000-04-30  
 PRIOR APPLICATION NUMBER: 08/600,273  
 PRIOR FILING DATE: 1996-02-08  
 PRIOR APPLICATION NUMBER: 08/486,820  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/385,540  
 PRIOR FILING DATE: 1995-02-08  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 20  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (1) ..(25)  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 US-09-549-642-20

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RESULT 6  
 Sequence 1 Application US/09644022A  
 GENERAL INFORMATION:  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Cowling, Didier S.P.  
 APPLICANT: Hubbel, Jeffrey A.  
 APPLICANT: van de Wetering, Petra

Query Match 98.6%; Score 136; DB 5; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 1  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-644-022A-1

---

RESULT 7  
 Sequence 2 Application US/09549642  
 GENERAL INFORMATION:  
 APPLICANT: Phairson Medical, Inc.  
 APPLICANT: de Faire, Johan  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Kay, John  
 APPLICANT: Lindblom, Ragnvald  
 TITLE OF INVENTION: Removing Dental Plaque with Krill  
 FILE REFERENCE: 314572-101F  
 CURRENT APPLICATION NUMBER: US/09/549,642  
 CURRENT FILING DATE: 2000-04-14  
 PRIOR APPLICATION NUMBER: 09/303,375  
 PRIOR FILING DATE: 2000-04-30  
 PRIOR APPLICATION NUMBER: 08/600,273  
 PRIOR FILING DATE: 1996-02-08  
 PRIOR APPLICATION NUMBER: 08/486,820  
 PRIOR FILING DATE: 1995-06-07  
 PRIOR APPLICATION NUMBER: 08/385,540  
 PRIOR FILING DATE: 1995-02-08  
 NUMBER OF SEQ ID NOS: 20  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 20  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (1) ..(25)  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 US-09-549-642-20

---

RESULT 8  
 Sequence 1 Application US/09644022A  
 GENERAL INFORMATION:  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Cowling, Didier S.P.  
 APPLICANT: Hubbel, Jeffrey A.  
 APPLICANT: van de Wetering, Petra

Query Match 98.6%; Score 136; DB 5; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-13; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO 1  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphausia superba  
 US-09-644-022A-1

TITLE OF INVENTION: Treatment of Trauma  
FILE REFERENCE: 314572-103B  
CURRENT APPLICATION NUMBER: US/09/644,022A  
CURRENT FILING DATE: 2000-08-23  
NUMBER SEQ ID NOS: 17  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Panaeus vanameii  
US-09-644-022A-1

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGWEATPHSWHQAALEFDDMYF 25

RESULT 9  
US-09-549-642-3  
Sequence 3, Application US/09549642  
GENERAL INFORMATION:  
APPLICANT: Phairson Medical, Inc.  
APPLICANT: de Faire, Johan  
APPLICANT: Franklin, Richard L.  
APPLICANT: Kay, John  
APPLICANT: Lindblom, Ragnvald  
TITLE OF INVENTION: Removing Dental Plaque with Krill Enzymes  
FILE REFERENCE: 314572-101F  
CURRENT APPLICATION NUMBER: US/09/549,642  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 09/303,375  
PRIOR FILING DATE: 2000-04-30  
PRIOR APPLICATION NUMBER: 08/600,273  
PRIOR FILING DATE: 1996-02-08  
PRIOR APPLICATION NUMBER: 08/486,820  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/385,540  
PRIOR FILING DATE: 1995-02-08  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus vanameii  
US-09-549-642-3

Query Match 73.2%; Score 101; DB 5; Length 25;  
Best Local Similarity 72.0%; Pred. No. 2.9e-08;  
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGWEATPHSWHQAALEFDDMYF 25

RESULT 10  
US-09-644-022A-6  
Sequence 6, Application US/09644022A  
GENERAL INFORMATION:  
APPLICANT: Franklin, Richard L.  
APPLICANT: Cowling, Didier S.P.  
APPLICANT: Hubel, Jeffrey A.  
APPLICANT: van de Wetering, Petra  
TITLE OF INVENTION: Treatment of trauma  
FILE REFERENCE: 314572-103B  
CURRENT APPLICATION NUMBER: US/09/644,022A  
CURRENT FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus monodon chymotryptic  
US-09-644-022A-6

Query Match 65.9%; Score 91; DB 5; Length 25;  
Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPMQVGLFIDDMYF 25  
Db 1 IVGGWEATPHSWHQAALEFDDMYF 25

RESULT 8  
US-09-303-375A-3  
Sequence 3, Application US/09303375A  
GENERAL INFORMATION:  
APPLICANT: Johan R. de Faire  
APPLICANT: Richard L. Franklin  
APPLICANT: John Kay  
APPLICANT: Ragnvald Lindblom  
TITLE OF INVENTION: Multifunctional Enzyme  
FILE REFERENCE: 314572-101E  
CURRENT APPLICATION NUMBER: US/09/303,375A  
CURRENT FILING DATE: 1999-04-30  
PRIOR APPLICATION NUMBER: US 08/486,820  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/486,540  
PRIOR FILING DATE: 1995-02-08  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Panaeus vanameii  
US-09-303-375A-3

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

---

RESULT 11  
 US-09-303-375A-7  
 ; Sequence 7, Application US/09303375A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Johan R. de Faire  
 ; APPLICANT: Richard L. Franklin  
 ; APPLICANT: John Kay  
 ; APPLICANT: Ragnvald Lindblom  
 ; TITLE OF INVENTION: Multifunctional Enzyme  
 ; FILE REFERENCE: 314572-101E  
 ; CURRENT APPLICATION NUMBER: US/09/303,375A  
 ; CURRENT FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: US 08/486,820  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIORITY NUMBER: US 08/385,540  
 ; PRIORITY FILING DATE: 1995-02-08  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Panaeus monodon

US-09-303-375A-7

Query Match 65.9%; Score 91; DB 5; Length 25;  
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

---

RESULT 12  
 US-09-549-642-7  
 ; Sequence 7, Application US/095499642  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Phairson Medical, Inc.  
 ; APPLICANT: de Faire, Johan  
 ; APPLICANT: Franklin, Richard L.  
 ; APPLICANT: Kay, John  
 ; APPLICANT: Lindblom, Ragnvald  
 ; TITLE OF INVENTION: Removing Dental Plaque with Kriill  
 ; TITLE OF INVENTION: Enzymes  
 ; FILE REFERENCE: 314572-101F  
 ; CURRENT APPLICATION NUMBER: US/09/549,642  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 09/303,375  
 ; PRIOR FILING DATE: 2000-04-30  
 ; PRIOR APPLICATION NUMBER: 08/600,273  
 ; PRIOR FILING DATE: 1996-02-08  
 ; PRIOR APPLICATION NUMBER: 08/486,820  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIOR APPLICATION NUMBER: 08/385,540  
 ; PRIOR FILING DATE: 1995-02-08  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Panaeus monodon

US-09-549-642-7

Query Match 65.9%; Score 91; DB 5; Length 25;  
 Best Local Similarity 64.0%; Pred. No. 9.7e-07;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

---

RESULT 13  
 US-09-644-022A-7  
 ; Sequence 7, Application US/09644022A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Franklin, Richard L.  
 ; APPLICANT: Cowling, Didier S.P.  
 ; APPLICANT: Hubbel, Jeffrey A.  
 ; APPLICANT: van de Watering, Petra  
 ; TITLE OF INVENTION: Treatment of Trauma  
 ; FILE REFERENCE: 314572-103B  
 ; CURRENT APPLICATION NUMBER: US/09/644,022A  
 ; CURRENT FILING DATE: 2000-08-23  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Uca pugilator enzyme

US-09-644-022A-7

Query Match 64.5%; Score 89; DB 5; Length 25;  
 Best Local Similarity 64.0%; Pred. No. 2e-06;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 14  
 US-09-303-375A-8  
 ; Sequence 8, Application US/09303375A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Johann R. de Faire  
 ; APPLICANT: Richard L. Franklin  
 ; APPLICANT: John Kay  
 ; APPLICANT: Ragnvald Lindblom  
 ; TITLE OF INVENTION: Multifunctional Enzyme  
 ; FILE REFERENCE: 314572-101E  
 ; CURRENT APPLICATION NUMBER: US/09/303,375A  
 ; CURRENT FILING DATE: 1999-04-30  
 ; PRIORITY NUMBER: US 08/486,820  
 ; PRIOR FILING DATE: 1995-06-07  
 ; PRIORITY NUMBER: US 08/385,540  
 ; PRIOR FILING DATE: 1995-02-08  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SEQ ID NO 8  
 ; LENGTH: 25  
 ; TYPE: PRT  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; ORGANISM: Uca pugilator

US-09-303-375A-8

Query Match 64.5%; Score 89; DB 5; Length 25;  
 Best Local Similarity 64.0%; Pred. No. 2e-06;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

RESULT 15  
 US-09-549-642-8  
 ; Sequence 8, Application US/095499642  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Phairson Medical, Inc.  
 ; APPLICANT: de Faire, Johan  
 ; APPLICANT: Franklin, Richard L.

APPLICANT: Kay, John  
APPLICANT: Lindblom, Ragnvald  
TITLE OF INVENTION: Removing Dental Plaque with Krill Enzymes  
FILE REFERENCE: 314572-1.01F  
CURRENT APPLICATION NUMBER: US/09/549,642.  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 09/303,375  
PRIOR FILING DATE: 2000-04-30  
PRIOR APPLICATION NUMBER: 08/600,273  
PRIOR FILING DATE: 1996-02-08  
PRIOR APPLICATION NUMBER: 08/486,820  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/385,540  
PRIOR FILING DATE: 1995-02-08  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Uca pugilator  
9-549-642-8

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Query Match      64.5%; Score 89; DB 5; Length 25;
Best Local Similarity 64.0%; Preq. No. 2e-06;
Matches 16; Conservative 3; Mismatches 6; Indels 0;
Gaps 0;

1 IVGGXEVTPHAYPWQVGLFDDMF 25
1 I|||||VGGXEVTPHAYPWQVGLFDDMF . .
1 IVGGXEVTPHAYPWQVGLFDDMF 25
1 IVGGXEVTPHAYPWQVGLFDDMF 25

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Search completed: May 30, 2003, 11:12:20  
Search time : 89 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 11:01:13 ; Search time 26 Seconds

(without alignments)  
28.291 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

number of hits satisfying chosen parameters:

262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*

2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*

3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep.\*

4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep.\*

5: /cgn2\_6/ptodata/1/1aa/SPECTUS-COMB.pep.\*

6: /cgn2\_6/ptodata/1/1aa/backfls1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	136	98.6	25	2	US-09-385-540A-1	Sequence 1, Appli
2	136	98.6	25	2	US-09-385-540A-2	Sequence 2, Appli
3	136	98.6	25	2	US-09-385-540A-17	Sequence 17, Appli
4	136	98.6	25	2	US-09-600-213A-1	Sequence 1, Appli
5	136	98.6	25	2	US-09-600-273A-2	Sequence 2, Appli
6	136	98.6	25	2	US-09-600-273A-17	Sequence 17, Appli
7	136	98.6	25	3	US-09-886-820-1	Sequence 1, Appli
8	136	98.6	25	3	US-09-886-820-2	Sequence 2, Appli
9	136	98.6	25	3	US-09-886-820-17	Sequence 17, Appli
10	136	98.6	25	3	US-09-8705-875A-19	Sequence 19, Appli
11	136	98.6	25	4	US-09-820-731-1	Sequence 1, Appli
12	136	98.6	25	4	US-09-220-731-2	Sequence 2, Appli
13	136	98.6	25	4	US-09-220-731-20	Sequence 20, Appli
14	136	98.6	178	3	US-09-705-875A-8	Sequence 8, Appli
15	136	98.6	178	4	US-09-220-731-23	Sequence 24, Appli
16	136	98.6	178	4	US-09-220-731-24	Sequence 19, Appli
17	136	98.6	300	3	US-09-705-875A-4	Sequence 4, Appli
18	136	98.6	300	3	US-09-705-875A-6	Sequence 6, Appli
19	136	98.6	300	4	US-09-220-731-21	Sequence 21, Appli
20	136	98.6	302	4	US-09-220-731-26	Sequence 26, Appli
21	123	89.1	23	4	US-09-220-731-19	Sequence 19, Appli
22	101	73.2	25	2	US-09-886-820-3	Sequence 3, Appli
23	101	73.2	25	2	US-09-886-820-3	Sequence 3, Appli
24	101	73.2	25	2	US-09-886-820-3	Sequence 3, Appli
25	101	73.2	25	3	US-09-220-731-3	Sequence 3, Appli
26	101	73.2	25	4	US-09-220-731-25	Sequence 25, Appli
27	96	211	4	US-09-220-731-25		

28	91	65.9	25	2	US-09-385-540A-7	Sequence 7, Appli
29	91	65.9	25	3	US-09-600-213A-7	Sequence 7, Appli
30	91	65.9	25	4	US-09-486-520-7	Sequence 7, Appli
31	91	65.9	25	4	US-09-220-731-7	Sequence 7, Appli
32	89	64.5	25	2	US-09-385-540A-8	Sequence 8, Appli
33	89	64.5	25	3	US-09-600-213A-8	Sequence 8, Appli
34	89	64.5	25	3	US-09-486-520-8	Sequence 8, Appli
35	89	64.5	25	4	US-09-220-731-8	Sequence 8, Appli
36	89	64.5	226	1	US-09-650-129-4	Sequence 4, Appli
37	89	64.5	226	3	US-09-984-417-4	Sequence 4, Appli
38	89	64.5	255	1	US-09-650-129-5	Sequence 5, Appli
39	89	64.5	255	3	US-09-984-417-5	Sequence 5, Appli
40	80	58.0	25	2	US-09-385-540A-6	Sequence 6, Appli
41	80	58.0	25	2	US-09-600-273A-6	Sequence 6, Appli
42	80	58.0	25	3	US-09-486-520-6	Sequence 6, Appli
43	80	58.0	25	4	US-09-220-731-6	Sequence 6, Appli
44	74	53.6	278	1	US-09-392-928C-4	Sequence 4, Appli
45	74	53.6	278	3	US-09-330-945-4	Sequence 4, Appli

#### ALIGNMENTS

RESULT 1	US-09-385-540A-1					
	Sequence 1, Application US/08385540A					
	Patent No. 5945102					
	GENERAL INFORMATION:					
	APPLICANT: de Faire, Johan					
	TITLE OF INVENTION: Wound Care With Multifunctional					
	NUMBER OF SEQUENCES: 20					
	CORRESPONDENCE ADDRESS:					
	ADDRESS: Dechert Price & Rhoads					
	STREET: 997 Lenox Drive, Building 3, Suite 210					
	CITY: Lawrenceville					
	STATE: NJ					
	COUNTRY: USA					
	ZIP: 08543					
	COMPUTER READABLE FORM:					
	MEDIUM TYPE: Diskette					
	COMPUEUR: IBM Compatible					
	OPERATING SYSTEM: Windows 95					
	SOFTWARE: PostSeq for Windows Version 2.0b					
	CURRENT APPLICATION DATA:					
	APPLICATION NUMBER: US/09-385,540A					
	FILING DATE:					
	CLASSIFICATION: 424					
	PRIOR APPLICATION DATA:					
	APPLICATION NUMBER: 08/600,273					
	FILING DATE: 08-FEB-1996					
	ATTORNEY/AGENT INFORMATION:					
	NAME: Bloom, Allen					
	REGISTRATION NUMBER: 29,135					
	REFERENCE/DOCKET NUMBER: 314572-101A					
	TELECOMMUNICATION INFORMATION:					
	TELEPHONE: 609-520-3214					
	TELEX:					
	INFORMATION FOR SEQ ID NO: 1:					
	SEQUENCE CHARACTERISTICS:					
	LENGTH: 25 amino acids					
	TYPE: amino acid					
	STRANDEDNESS: single					
	TOPOLOGY: linear					
	US-09-385-540A-1					
	Query Match	98.6%	Score 136;			
	Best Local Similarity	96.0%	Pred. No. 3.5e-15;			
	Matches	24;	Conservative	0;	Mismatches	1;
					Indels	0;
					Gaps	0;
Qy	1 IVGGXEVTPHAYPWQVGLFIDMF	25				

1 VEGGENETPHARYMOVGLIEIDMMYF 25 DB

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-620-1214  
TELEFAX: 609-620-3239  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-600-273A-1

Query Match 98.6%;  
Best Local Similarity 96.0%;  
Matches 24; Conservative 0;

Dy [REDACTED] RT 5  
Ddb [REDACTED]

1 I VGGXEVTPHAYPKQVGLFID	1 I VGGNEVTPHAYPKQVGLFID
--------------------------	--------------------------

JS-08-600-273A-2  
Sequence 2, Application US/086002  
Patent No. 5956406  
GENERAL INFORMATION:  
APPLICANT: de Faire, Johan  
APPLICANT: Franklin, Richard  
APPLICANT: Kay, John  
TITLE OF INVENTION: Acne Treata  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dechert Price &  
STREET: 997 Lenox Drive, Bu  
CITY: Lawrenceville  
STATE: NJ  
COUNTRY: USA  
ZIP: 08543  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 9  
SOFTWARE: FastSEQ for Window  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/6  
FILING DATE: 08-FEB-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 0/0/06/  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 0/385/  
FILING DATE: 08-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bloom, Allen  
REGISTRATION NUMBER: 29-135  
REFERENCE/DOCKET NUMBER: 31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-620-3214  
TELEFAX: 609-620-3259  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-600-273A-2

Query Match 98.6%;  
Best Local Similarity 96.0%;  
Matches 24; Conservative 0;

Qy 1 IVGGXEVTPHAYPQVGFLDDMYF 25  
 US-08-600-273A-17  
 ; Sequence 17, Application US/08600273A  
 ; Patent No. 5958406  
 Db 1 IVGGMETVTPHAYPQVGFLDDMYF 25

**RESULT 6**

Qy 1 IVGGXEVTPHAYPQVGFLDDMYF 25  
 US-08-600-273A-17  
 ; Sequence 17, Application US/08600273A  
 ; Patent No. 5958406  
 Db 1 IVGGMETVTPHAYPQVGFLDDMYF 25

; GENERAL INFORMATION:  
 ; APPLICANT: de Faire, Johan L.  
 ; APPLICANT: Kay, John  
 ; TITLE OF INVENTION: Acne Treatment With Multifunctional  
 ; TITLE OF INVENTION: Enzyme  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Dechert Price & Rhoads  
 ; STREET: 997 Lenox Drive, Building 3, Suite 210  
 ; CITY: Lawrenceville  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 08543  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: FastSEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/600,273A  
 ; FILING DATE: 08-FEB-1996  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/486,820  
 ; FILING DATE: 07-JUN-1995  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/385,540  
 ; FILING DATE: 08-FEB-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bloom, Allen  
 ; REGISTRATION NUMBER: 29,135  
 ; REFERENCE/DOCKET NUMBER: 314572-101C  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 609-520-3214  
 ; TELEFAX: 609-620-3259  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 25 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-600-273A-17

Query Match 98.6%; Score 136; DB 2; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0

Qy 1 IVGGXEVTPHAYPQVGFLDDMYF 25  
 Db 1 IVGGMETVTPHAYPQVGFLDDMYF 25

**RESULT 7**

Qy 1 IVGGXEVTPHAYPQVGFLDDMYF 25  
 US-08-486-820-1  
 ; Sequence 1, Application US/08486820  
 ; Patent No. 6030612  
 ; GENERAL INFORMATION:  
 ; APPLICANT: de Faire, Johan L.  
 ; APPLICANT: Franklin, Richard L.  
 ; APPLICANT: Kay, John  
 ; TITLE OF INVENTION: Antimicrobial Uses Of Multifunctional

TITLE OF INVENTION: Enzyme  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dechart Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,820  
 FILING DATE:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/486,820  
 FILING DATE: 07-JUNE-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BLOOM, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER: 314572-101B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-620-3214  
 TELEFAX: 609-620-3259  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-486-820-1

Query Match 98.6%; Score 136; DB 3; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 3.5e-15; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPNOVGLFDDMF 25  
 Db 1 IVGGNEVTPHAYPNOVGLFDDMF 25

---

RESULT 8  
 US-08-486-820-2  
 Sequence 2, Application US/08486820  
 Patent No: 6030612  
 GENERAL INFORMATION:  
 APPLICANT: de Faire, Johan  
 APPLICANT: Franklin, Richard L.  
 TITLE OF INVENTION: Enzyme  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dechart Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,820  
 FILING DATE: 07-JUNE-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BLOOM, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER: 314572-101B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-620-3214  
 TELEFAX: 609-620-3259  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-486-820-17

Query Match 98.6%; Score 136; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

RESULT 10  
 US-08-705-875A-19  
 Sequence 19, Application US/08705875A

Patent No. 6040155

GENERAL INFORMATION:  
 APPLICANT: Kille, Peter  
 TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING  
 TITLE OF INVENTION: SAME  
 NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
 ADDRESS: Dechert Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08543

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/04/705,875A  
 FILING DATE: 28-AUG-1996  
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/768,318  
 FILING DATE: 17-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bloom, Allen  
 REGISTRATION NUMBER: 29,135  
 REFERENCE/DOCKET NUMBER: 314572-102US

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 609-520-1214  
 TELEX:

INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 25 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

Query Match 98.6%; Score 136; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

RESULT 11  
 US-09-220-731-1  
 Sequence 1, Application US/09220731A

Patent No. 6232088

GENERAL INFORMATION:  
 APPLICANT: Phalison Medical, Inc.  
 APPLICANT: Richard L. Franklin  
 APPLICANT: Yves St. Pierre

TITLE OF INVENTION: Treatment and Prevention of Immune

FILE REFERENCE: 314572-101D

CURRENT APPLICATION NUMBER: US/09/220,731A  
 FILING DATE: 1998-12-24  
 EARLIER APPLICATION NUMBER: PCT/SE93/00455  
 EARLIER FILING DATE: 1993-05-21  
 EARLIER APPLICATION NUMBER: 08/338,501  
 EARLIER FILING DATE: 1994-11-22  
 EARLIER APPLICATION NUMBER: 08/385,540  
 EARLIER FILING DATE: 1995-02-08  
 NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 1  
 LENGTH: 25  
 TYPE: PRT  
 ; ORGANISM: Euphasia superba

US-09-220-731-1

Query Match 98.6%; Score 136; DB 4; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

Query Match 98.6%; Score 136; DB 4; Length 25;  
 Best Local Similarity 96.0%; Pred. No. 3.e-15; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

RESULT 13  
 US-09-220-731-20

TITLE OF INVENTION: Treatment and Prevention of Immune

Sequence 20, Application US/09220731A  
 GENERAL INFORMATION:  
 APPLICANT: Phairson Medical, Inc.  
 APPLICANT: Richard L. Franklin  
 APPLICANT: Yves St. Pierre  
 TITLE OF INVENTION: Treatment and Prevention of Immune Rejection Reactions  
 FILE REFERENCE: 314572-101D  
 CURRENT APPLICATION NUMBER: US/09/220,731A  
 CURRENT FILING DATE: 1998-12-24  
 EARLIER APPLICATION NUMBER: PCT/SE93/00455  
 EARLIER FILING DATE: 1993-05-21  
 EARLIER APPLICATION NUMBER: 08/338,501  
 EARLIER FILING DATE: 1994-11-22  
 EARLIER APPLICATION NUMBER: 08/385,540  
 EARLIER FILING DATE: 1995-02-08  
 EARLIER APPLICATION NUMBER: 08/486,820  
 EARLIER FILING DATE: 1995-06-07  
 EARLIER APPLICATION NUMBER: 08/600,273  
 EARLIER FILING DATE: 1996-02-08  
 NUMBER OF SEQ ID NOS: 26  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 20  
 LENGTH: 25  
 TYPE: PRT  
 ORGANISM: Euphasia superba  
 FEATURE:  
 NAME/KEY: VARIANT  
 LOCATION: (5)...(5)  
 OTHER INFORMATION: xaa = Any Amino Acid  
 US-09-220-731-20

Query Match 98.6%; Score 136; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-15;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPQVGLFIDDMYF 25  
 Db 1 IVGGXEVTPHAYPQVGLFIDDMYF 25

RESULT 14  
 US-08-705-875A-8  
 Sequence 8, Application US/08705875A  
 GENERAL INFORMATION:  
 APPLICANT: Key, John  
 APPLICANT: Kille, Peter  
 TITLE OF INVENTION: ENZYME AND DNA SEQUENCE ENCODING  
 TITLE OF INVENTION: SAME  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Decher Price & Rhoads  
 STREET: 997 Lenox Drive, Building 3, Suite 210  
 CITY: Lawrenceville  
 STATE: NJ  
 ZIP: 08543  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: FastSeq for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/705,875A  
 FILING DATE: 28-AUG-1996  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/768,318  
 FILING DATE: 17-DEC-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bloom, Allen

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OM protein - protein search, using sw model.

Run on: May 30, 2003, 11:04:17 ; Search time 45 Seconds (without alignments)

56,235 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGGMEVTPHAYPAVGVLFDDMF 25

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Searched: 383519 seqs, 101223694 residues

number of hits satisfying chosen parameters: 383519

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA:  
 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:  
 2: /cgn2\_6/ptodata/1/pubpaa/US07\_PUB.pep:  
 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:  
 4: /cgn2\_6/ptodata/1/pubpaa/US05\_PUBCOMB.pep:  
 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:  
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 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:  
 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:  
 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:  
 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:  
 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:  
 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:  
 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	136	98.6	300	9	US-09-938-269-1	Sequence 1, Appli
2	101	73.2	25	9	US-09-938-269-2	Sequence 2, Appli
3	91	65.9	25	9	US-09-938-269-6	Sequence 6, Appli
4	89	64.5	25	9	US-09-938-269-7	Sequence 7, Appli
5	80	58.0	25	9	US-09-938-269-5	Sequence 5, Appli
6	75.5	54.7	970	10	US-09-888-615-101	Sequence 101, Appli
7	70	50.7	272	9	US-10-117-323-37	Sequence 37, Appli
8	69	50.0	271	9	US-10-117-323-39	Sequence 39, Appli
9	68	49.3	20	9	US-09-938-269-3	Sequence 3, Appli
10	67	48.6	252	9	US-10-117-323-38	Sequence 38, Appli
11	66	47.8	229	9	US-09-898-837A-53	Sequence 53, Appli
12	66	47.8	260	9	US-09-978-295A-395	Sequence 395, App
13	66	47.8	260	9	US-09-978-697-395	Sequence 395, App
14	66	47.8	260	9	US-09-978-192A-395	Sequence 395, App
15	66	47.8	260	9	US-09-999-832A-395	Sequence 395, App
16	66	47.8	260	9	US-09-978-189-395	Sequence 395, App
17	66	47.8	260	9	US-10-028-072-396	Sequence 396, App
18	66	47.8	260	9	US-10-121-049-396	Sequence 396, App
19	66	47.8	260	9	US-10-123-904-396	Sequence 396, App

**ALIGNMENTS**

RESULT	1	US-09-938-269-1	;	Sequence 1, Application US-09988269	
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	Publication No. US20030007951A1
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	GENERAL INFORMATION:
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Franklin, Richard L.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Cowling, Didier S.P.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Hubbel, Jeffrey A.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: van de Wetering, Petra
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	FILE REFERENCE: 314572-105
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	CURRENT APPLICATION NUMBER: US/09/938,269
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	CURRENT FILING DATE: 2001-08-23
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	NUMBER OF SEQ ID NOS: 17
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	SOFTWARE: FastSEQ for Windows Version 4.0
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	SEQ ID NO: 1
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	LENGTH: 300
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	TYPE: PRT
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	ORGANISM: Panaeu vanamei
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	US-09-938-269-1

**RESULT**

RESULT	2	US-09-938-269-2	;	Sequence 2, Application US-09988269	
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	Publication No. US20030007951A1
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	GENERAL INFORMATION:
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Franklin, Richard L.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Cowling, Didier S.P.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: Hubbel, Jeffrey A.
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	APPLICANT: van de Wetering, Petra
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	FILE REFERENCE: 314572-105
QY	1	IVGGMEVTPHAYPAVGVLFDDMF	25	;	CURRENT APPLICATION NUMBER: US/09/938,269

CURRENT FILING DATE: 2001-08-23  
 NUMBER OF SEQ ID NOs: 17  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 2

LENGTH: 25

TYPE: PRT ; ORGANISM: Panaeus vanamei  
 US-09-938-269-2

Query Match Best Local Similarity 73.2%; Score 101; DB 9; Length 25;  
 Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWNQVGLFTDDMF 25  
 Db 1 IVGGYEATPHSWPQAAFLFTDDMF 25

LNT 3  
 [REDACTED] 6  
 Publne 6, Application US/09938269

GENERAL INFORMATION:  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Cowling, Didier S.P.  
 APPLICANT: Hubbel, Jeffrey A.  
 APPLICANT: van de Wetering, Petra  
 TITLE OF INVENTION: Treatment of Trauma  
 FILE REFERENCE: 314572-105  
 CURRENT APPLICATION NUMBER: US/09/938,269  
 CURRENT FILING DATE: 2001-08-23  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 6

LENGTH: 25

TYPE: PRT ; ORGANISM: Panaeus monodon chymotryptic  
 US-09-938-269-6

Query Match Best Local Similarity 60.0%; Score 80; DB 9; Length 25;  
 Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWNQVGLFTDDMF 25  
 Db 1 IVGGYEAVPGWNPYQAAFLFTDDMF 25

RESULT 5  
 US-09-938-269-5

Sequence 5, Application US/09938269  
 Publication No. US20030007951A1.  
 GENERAL INFORMATION:  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Cowling, Didier S.P.  
 APPLICANT: Hubbel, Jeffrey A.  
 APPLICANT: van de Wetering, Petra  
 TITLE OF INVENTION: Treatment of Trauma  
 FILE REFERENCE: 314572-105  
 CURRENT APPLICATION NUMBER: US/09/938,269  
 CURRENT FILING DATE: 2001-08-23  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 5

LENGTH: 25

TYPE: PRT ; ORGANISM: Panaeus monodon chymotryptic  
 US-09-938-269-5

Query Match Best Local Similarity 60.0%; Score 80; DB 9; Length 25;  
 Matches 15; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWNQVGLFTDDMF 25  
 Db 1 IVGGYEAVPGWNPYQAAFLFTDDMF 25

RESULT 6  
 US-09-888-615-101

Sequence 101, Application US/09888615  
 Patent No. US20020064856A1  
 GENERAL INFORMATION:  
 APPLICANT: PLOWMAN, GREGORY  
 APPLICANT: WHYTE, DAVID  
 APPLICANT: CAENEPEL, SEAN  
 APPLICANT: CHAROCZAK, GLEN  
 APPLICANT: MANNING, GERARD  
 APPLICANT: SUDARSANAM, SUCHA  
 TITLE OF INVENTION: NOVEL PROTEASES  
 FILE REFERENCE: 038602/1214  
 CURRENT APPLICATION NUMBER: US/09/888,615  
 CURRENT FILING DATE: 2001-06-26  
 PRIOR APPLICATION NUMBER: 60/214,047  
 NUMBER OF SEQ ID NOS: 150  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 101  
 LENGTH: 970

TYPE: PRT ; ORGANISM: Homo sapiens  
 US-09-888-615-101

Query Match Best Local Similarity 60.9%; Score 75.5; DB 10; Length 970;  
 Matches 14; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 1 IVGGXEVTPHAYPWNQVGL-FIDD 22  
 Db 433 IAGGEACPHCPWQVGLRFGLD 455

RESULT 7  
 US-10-117-323-37

Sequence 7, Application US/09938269  
 Publication No. US20030007951A1  
 GENERAL INFORMATION:  
 APPLICANT: Franklin, Richard L.  
 APPLICANT: Cowling, Didier S.P.  
 APPLICANT: Hubbel, Jeffrey A.  
 APPLICANT: van de Wetering, Petra  
 TITLE OF INVENTION: Treatment of Trauma  
 FILE REFERENCE: 314572-105  
 CURRENT APPLICATION NUMBER: US/09/938,269  
 CURRENT FILING DATE: 2001-08-23  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 7

LENGTH: 25

TYPE: PRT ; ORGANISM: Uca pugilator enzyme  
 US-09-938-269-7

Query Match Best Local Similarity 64.0%; Score 89; DB 9; Length 25;  
 Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Page 3

; GENERAL INFORMATION:  
 ; APPLICANT: Rancourt, Derrick E.  
 ; APPLICANT: Rancourt, Susan L.  
 ; APPLICANT: O'Sullivan, Colleen M.  
 ; TITLE OF INVENTION: Implantation Serine Proteinases  
 ; FILE REFERENCE: 033337-005  
 ; CURRENT APPLICATION NUMBER: US/10/117,323  
 ; CURRENT FILING DATE: 2002-04-08  
 ; PRIOR APPLICATION NUMBER: US 60/281,724  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/294,736  
 ; PRIOR FILING DATE: 2001-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/350,962  
 ; PRIOR FILING DATE: 2002-01-25  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 37  
 ; LENGTH: 272  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ; US-10-117-323-37

Query Match 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Best Local Similarity 48.0%; Pred. No. 0.0055; Length 272;  
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Query Match 29 IVGGQEASGNWPWQSLRNDTYW 53  
 Best Local Similarity 48.0%; Pred. No. 0.0055; Length 272;  
 Matches 12; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

**RESULT 8**  
 US-10-117-323-39  
 Sequence 39, Application US/10117323  
 ; Publication No. US20030054993A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rancourt, Derrick E.  
 ; APPLICANT: Rancourt, Susan L.  
 ; APPLICANT: O'Sullivan, Colleen M.  
 ; TITLE OF INVENTION: Implantation Serine Proteinases  
 ; FILE REFERENCE: 033337-005  
 ; CURRENT APPLICATION NUMBER: US/10/117,323  
 ; CURRENT FILING DATE: 2002-04-08  
 ; PRIOR APPLICATION NUMBER: US 60/281,724  
 ; PRIOR FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: US 60/350,962  
 ; PRIOR FILING DATE: 2002-01-25  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 38  
 ; LENGTH: 252  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ; US-10-117-323-38

Query Match 1 IVGGXEVTPHAYPWQVGL 18  
 Best Local Similarity 50.0%; Pred. No. 0.0077; Length 271;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Query Match 31 IVGGQEATPNWPWQVSL 48  
 Best Local Similarity 61.1%; Pred. No. 0.0077; Length 271;  
 Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

**RESULT 9**  
 US-09-938-269-3  
 Sequence 3, Application US/09938269  
 ; Publication No. US2003007951A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Franklin, Richard L.  
 ; APPLICANT: Cowling, Didier S.P.  
 ; APPLICANT: Burgess, Catherine L.  
 ; APPLICANT: Herrmann, John L.  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Kumud, Maumder  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Quinn, Kerry E.  
 ; APPLICANT: Publican, Quinon  
 ; APPLICANT: Hervet, Daniel  
 ; APPLICANT: US-09-938-269-3  
 ; Sequence 53, Application US/09898837A  
 ; Publication No. US20030077697A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Kumud, Maumder  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Quinn, Kerry E.  
 ; APPLICANT: Publican, Quinon  
 ; APPLICANT: Hervet, Daniel

APPLICANT: Fernandes, Elma  
 APPLICANT: Taupier Jr., Raymond  
 APPLICANT: Rastelli, Luca  
 APPLICANT: CurGen Corporation  
 APPLICANT: Gerlach, Valerie L  
 APPLICANT: Macdougal, John L  
 TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND NUCLEAR ACIDS ENCODING THE SAME  
 FILE REFERENCE: 15966-598 CIP  
 CURRENT APPLICATION NUMBER: US/09/898,837A  
 CURRENT FILING DATE: 2001-07-03  
 PRIORITY NUMBER: U.S.S.N. 60/165,986  
 PRIOR FILING DATE: 1999-11-17  
 PRIORITY NUMBER: U.S.S.N. 60/194,839  
 PRIOR FILING DATE: 2000-04-05  
 PRIORITY NUMBER: U.S.S.N. 60/195,637  
 PRIOR FILING DATE: 2000-04-07  
 PRIORITY NUMBER: U.S.S.N. 60/197,080  
 PRIOR FILING DATE: 2000-04-13  
 PRIORITY NUMBER: U.S.S.N. 60/232,677  
 PRIOR FILING DATE: 2000-09-15  
 PRIORITY NUMBER: U.S.S.N. 60/181,347  
 PRIOR FILING DATE: 2000-02-09  
 PRIORITY NUMBER: U.S.S.N. 60/194,195  
 PRIOR FILING DATE: 2000-04-03  
 PRIORITY NUMBER: U.S.S.N. 60/215,906  
 PRIOR FILING DATE: 2000-07-03  
 PRIORITY NUMBER: U.S.S.N. 09/715,427  
 PRIOR FILING DATE: 2000-11-16  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 53  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-898-837A-53

Query Match 47 8%; Score 66; DB 9; Length 229;  
 Best Local Similarity 45.8%; Pred. No. 0.019;  
 Matches 11; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy	1 IVGGXEVTPHAYPHQVQLFIDDMY 24
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RESULT 12  
 9-978-295A-395  
 Invenue 395, Application US/09978295A  
 Patent No. US20020156006A1

GENERAL INFORMATION:

- APPLICANT: Ashkenazi, Avi
- APPLICANT: Baker, Kevin P.
- APPLICANT: Botstein, David
- APPLICANT: Desnoyers, Luc
- APPLICANT: Eaton, Dan
- APPLICANT: Ferrara, Napoleon
- APPLICANT: Filvaroff, Ellen
- APPLICANT: Fong, Sherman
- APPLICANT: Gao, Wei-Qiang
- APPLICANT: Gerber, Hanspeter
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Grimaldi, J. Christopher
- APPLICANT: Gurney, Austin L.
- APPLICANT: Hillan, Kenneth J
- APPLICANT: Klaavio, Ivar J.
- APPLICANT: Kuo, Sophia S.
- APPLICANT: Napier, Mary A.
- APPLICANT: Pan, James
- APPLICANT: Paoni, Nicholas F.
- APPLICANT: Roy, Margaret Ann

PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
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; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1 IVGGXEVTPHAYPVOGLF 19  
Best Local Similarity 52.6% ; Score 66; DB 9; Length 260;  
Matches 10; Conservative 3; Mismatches 6; Indels 0; Caps 0;

Qy Db

RESULT 13 US-09-978-697-395  
; Sequence 395, Application US/09978697  
; Patent No. US20020169284A1  
GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Destroyer, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audley  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kjavian, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paonil, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Tumash, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William L.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

FILE REFERENCE: P2630P1C27  
CURRENT APPLICATION NUMBER: US/09/978,697  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR FILING DATE: 1997-11-21  
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PRIOR FILING DATE: 1998-04-08



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 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084643  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/085339  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085338  
 PRIOR FILING DATE: 1998-05-13  
 PRIOR APPLICATION NUMBER: 60/085323  
 PRIOR FILING DATE: 1998-05-13

Query Match 47.8% Score 66; DB 9; Length 260;  
 Best Local Similarity 52.6%; Pred. No. 0.021;  
 Matches 10; Conservative 3; Mismatches 6; Indels 0;  
 Gaps 0;

Qy 1. IVGGXETPHAYPWQVGLF 19  
 Db 33 VLGGECPHSOPWQAALF 51

RESULT 15  
 US-09-999-832A-395  
 Sequence 395, Application US/09999832A  
 Publication No. US20020192706A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillman, Kenneth J.  
 APPLICANT: Klijavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, Nicholas F.  
 APPLICANT: Paon, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane PolyPeptides and Nucleic  
 FILE REFERENCE: P2630PIC63  
 CURRENT FILING DATE: US/09/999-832A  
 PRIOR APPLICATION NUMBER: 09/916585  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: 09/916585  
 PRIOR FILING DATE: 2001-10-24  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/062449  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/077450



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Page 10

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Query Match 47.88; Score 66; DB 9; Length 260;  
Best Local Similarity 52.68; Pred. No. 0.021; Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYFWQVGLF 19  
Db 33 VLGGHECCPHSQFWQAAIF 51

Search completed: May 30, 2003, 11:13:13  
Time : 46 secs

Copyright (c) 1993 - 2003	GenCore version 5.1.6	Compugen Ltd.			
protein - protein search, using sw mode!					
on: May 30, 2003, 10:50:27 ; Search time 22 Seconds (without alignments) 47.132 Million cell updates/sec					
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effect score: 138					
Sequence: 1 IVGGEVTPHAYPWQVGLFDDMF 25					
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gapop 10.0 , Gapext 0.5					
searched: 112892 seqs, 41476328 residues	112892				
number of hits satisfying chosen parameters:					
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
Stat-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database : SwissProt_40:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
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No.	Score	Match	Length	DB	ID
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2	101	73.2	271	1	CTRL2_PENVA
3	89	64.5	226	1	COGS_ICAPU
4	80	58.0	31	1	CTRP_PENMO
5	70	50.7	273	1	MCT7_RAT
6	69	50.0	271	1	EL2_MOUSE
7	69	50.0	343	1	PLMN_SHEEP
8	67	48.6	245	1	CTRB_GADMO
9	67	48.6	268	1	CLCR_HUMAN
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4	65	47.1	20	1	COGL_CHTOPO
5	65	47.1	262	1	GRAA_HUMAN
6	64	46.4	269	1	EL2A_HUMAN
7	63	45.7	20	1	COGL_PARCM
8	63	45.7	269	1	EL2_PIG
9	63	45.7	273	1	MCT7_MOUSE
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4	63	45.7	812	1	PLMN_MOUSE
5	63	45.7	1420	1	APOA_MACMU
6	63	45.7	4548	1	APOA_HUMAN
7	62	44.9	254	1	KLK4_HUMAN
8	62	44.9	268	1	CLCR_RAT
9	62	44.9	810	1	PLMN_HUMAN
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1	61	44.2	269	1	EL2_BOVIN
2	61	44.2	810	1	PLMN_MACMU
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4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	9872	1	ENTK_MACLA
2	61	44.2	1035	1	ENTK_MACLA
3	61	44.2	9872	1	ENTK_MACLA
4	61	44.2	1035	1	ENTK_MACLA
5	61	44.2	9872	1	ENTK_MACLA
6	61	44.2	1035	1	ENTK_MACLA
7	61	44.2	9872	1	ENTK_MACLA
8	61	44.2	1035	1	ENTK_MACLA
9	61	44.2	9872	1	ENTK_MACLA
0	61	44.2	1035	1	ENTK_MACLA
1	61	44.2	98		





FT	DISULFID	218	246	BY SIMILARITY.	FT	DISUFLID	188	204	BY SIMILARITY.
FT	CARBOHYD	49	49	N-LINKED (GLCNAC, . ) (PROBABLE).	FT	DISUFLID	214	245	BY SIMILARITY.
FT	CONFLICT	42	42	W -> V (IN REF. 3).	FT	DISUFLID	271 AA;	281913 MW;	FAS42AE38FED3B4B CRC64;
FT	CONFICT	49	51	NDT -> WLP (IN REF. 3).	FT	SEQUENCE	271 AA;		
SQ	SEQUENCE	273 AA;	30400 MW;	65A5ED4D279FB284 CRC64;					
Query Match	50.7%	Score 70;	DB 1;	Length 273;	Query Match	50.0%	Score 69;	DB 1;	Length 271;
Best Local Similarity	48.0%	Pred. No.	0.0027		Best Local Similarity	61.1%	Pred. No.	0.0037	
Matches	12;	Conservative	6;	Mismatches	7;	Indels	0;	Gaps	0;
Qy	1	IVGGXEVTPHAYPNQVGLFDNYF 25			Qy	1	IVGGXEVTPHAYPNQVGL	18	
Db	29	IVGGQEASGNKWPQVSRLRVNDIYW 53			Db	31	VVGGOBATPNTWPWVYSL 48		
	RESULT 6				RESULT 7				
	EL2_MOUSE				PLMN_SHEEP				
ID	EL2_MOUSE				ID	PLMN_SHEEP			
	STANDARD;				STANDARD;				
	PRT;				PRT;				
	271 AA.				343 AA.				
PO5208;	13-AUG-1987 (Rel. 05, Created)				RA	"Complete amino acid sequence of ovine mini-plasminogen."			
	13-AUG-1987 (Rel. 05, Last sequence update)				RT	Protein Seq. Data Anal. 5:21-25 (1992).			
	15-JUN-2002 (Rel. 41, Last annotation update)				-!	FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFILTRATION: IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE; IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.			
DE	ELASTase 2 precursor (EC 3.4.21.71).				-!	CATALYTIC ACTIVITY: Preferential cleavage: Lys-1-Xaa > Arg-1-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.			
GN	ELA2.				-!	ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.			
OS	Mus musculus (Mouse).				-!	MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.				-!	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. PLASMINOGEN SUBFAMILY.			
NCBI_TaxID=10090;	[1]				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RN	SEQUENCE FROM N.A.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RX	MEDLINE-87066713; PubMed=3641189;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RA	Stevenson B.J., Hagenbuchle O., Wellauer P.K.;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RT	"Sequence organisation and transcriptional regulation of the mouse elastase II and trypsin genes".				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RT	Elastase II and trypsin genes".				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
RL	Nucleic Acids Res 14:8307-8330(1986).				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-!- FUNCTION: ACTS UPON ELASTIN.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-1-Xaa and Phe-1-Xaa. Hydrolyzes elastin.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-!- SUBCELLULAR LOCATION: Secreted.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-!- TISSUE SPECIFICITY: PANCREAS.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	-----				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
CC	This SWISS-PROT entry is copy right. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch);				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	EMBL: X04573; CAA28242.1;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	EMBL: X04576; CAR2244.1;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PIR: A25528; A25528.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	HSSP: P00772; 1EUG.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	MEROPS: S01.155;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	MEROPS: S01.155;				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	MGI: 95116; Bla.2.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	InterPro: IPR01314. Chymotrypsin.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	InterPro: IPR0125. Serine_protease_tryp.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PF00089; trypsin_1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PRINT222; CHYMOTRYPSIN.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	SMART: SM00020; TRYSPC_1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PROSITE: PS00020; TRYSPC_1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PROSITE: PS0240; TRYPSIN_DOM; 1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PROSITE: PS0134; TRYPSIN_HIS; 1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
DR	PROSITE: PS00135; TRYPSIN_SER; 1.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
KW	Hydrolase; Serine protease; Zymogen; Signal.				CC	IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.			
FT*	SIGNAL	1	16	ACTIVATION PEPTIDE.	KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.			
FT*	PROPEL	17	30	ELASTASE 2.	KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.			
FT	CHAIN	31	271	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	NON-TER	1		
FT	ACT SITE	75	75	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	<1	HEAVY CHAIN A.	
FT	ACT SITE	123	123	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	141	>343	
FT	ACT SITE	218	218	CHARGE RELAY SYSTEM (BY SIMILARITY).	FT	DOMAIN	<1	LIGHT CHAIN A.	
FT	DISULFID	60	76	BY SIMILARITY.	FT	DOMAIN	120	17	
FT	DISULFID	157	224	BY SIMILARITY.	FT	DOMAIN	41	120	
					FT	DOMAIN	114	341	
					FT	DOMAIN			

FT ACT-SITE	181	181	CHARGE RELAY SYSTEM.
FT ACT-SITE	224	224	CHARGE RELAY SYSTEM.
FT ACT-SITE	319	319	CHARGE RELAY SYSTEM.
FT NON-TER	343	343	CHARGE RELAY SYSTEM.
SEQUENCE	343 AA:	37662 MW:	8DF6EBA92D596EE0 CRC64:
Query Match	50 0%;	Score 69; DB 1;	Length 343;
Best Local Similarity	61.1%;	Pred. No. 0.0047;	3; Mismatches 4; Indels 0;
Matches 11; Conservative			
Db	114 VVGGCVATPHSPWQVGL 18		
Db	114 VVGGCVATPHSPWQVSL 131		
RESULT 8			
CTRB_GADMO	STANDARD;	PRT;	245 AA.
ID CTRB_GADMO	STANDARD;	PRT;	245 AA.
AC P80616;	(Rel. 34, Created)		
DE 01-OCT-1996 (Rel. 34, Last sequence update)			
DE 15-JUN-2002 (Rel. 41, Last annotation update)			
Chymotrypsin B (EC 3.4.21.1).			
Gadus morhua (Atlantic cod).			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Actinopterygii; QC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.			
NCBI_TaxID=8049;			
SEQUENCE.			
TISSUE=Pyloric caeca;			
MEDLINE=96439045; PubMed=8841380;			
Leth-Larsen R., Asgeirsson B., Thorolfsson M., Moerregaard-Madsen M., RA Hoejrup P.;			
"Structure of chymotrypsin variant B from Atlantic cod, <i>Gadus morhua</i> ,"			
Biochim. Biophys. Acta 1297:49-56(1996).			
SEQUENCE OF 1-12 AND 16-31.			
TISSUE=Pyloric caeca;			
MEDLINE=9211125; PubMed=1764912;			
Asgeirsson B., Bjarnason J.B.; RA RT	"Structural and kinetic properties of chymotrypsin from Atlantic cod (Gadus morhua). Comparison with bovine chymotrypsin."		
Comp. Biochem. Physiol. 99B:327-335(1991).			
-I - CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Trp-1-Xaa, CC CC			
phe-1-Xaa, Leu-1-Xaa.			
-I - SUBCELLULAR LOCATION: Extracellular.			
HSSP; P00766; 1CHG.			
DR PRINTS; PR00722; CHYMOTRYPSIN.			
DR SMART; SM0020; TRY-SPC; 1.			
DR PROSITE; PS50240; TRYPSIN DOM; 1.			
DR PROSITE; PS00134; TRYPSIN HIS; 1.			
DR PROSITE; PS00135; TRYPSIN SER; 1.			
KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.			
FT CHAIN 1 13 CHYMOTRYPSIN B, A CHAIN.			
FT CHAIN 16 245 CHYMOTRYPSIN B, B CHAIN.			
FT ACT-SITE 57 57 CHARGE RELAY SYSTEM (BY SIMILARITY).			
FT ACT-SITE 101 101 CHARGE RELAY SYSTEM (BY SIMILARITY).			
FT ACT-SITE 195 195 CHARGE RELAY SYSTEM (BY SIMILARITY).			
FT DISULFID 1 121 BY SIMILARITY.			
FT DISULFID 42 58 BY SIMILARITY.			
FT DISULFID 135 201 BY SIMILARITY.			
FT DISULFID 167 182 BY SIMILARITY.			
FT DISULFID 191 220 BY SIMILARITY.			
FT CONFLICT 9 11 QVT > VIS (IN REF 2).			
FT CONFLICT 26 26 S > T (IN REF 2).			
FT CONFLICT 29 29 PW > Y (IN REF 2).			
RESULT 9			
CLCR_HUMAN STANDARD;			
ID CLCR_HUMAN ID: 000765;			
AC Q99895; Q9NUH5; 000765;			
DT 16-OCT-2001 (Rel. 40, Created)			
DT 16-OCT-2001 (Rel. 40, Last sequence update)			
DE Caldeocrin precursor (EC 3.4.21.2) (Chymotrypsin C).			
GN CTRC OR CLCR.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX NCBI_TAXID=9606;			
RN "Molecular cloning and expression of human caldeocrin.";			
RP SEQUENCE FROM N.A., AND VARIANT TRP-80.			
RC TISSUE=Pancreas;			
RX MEDLINE=9621165; PubMed=8635596;			
RA Tomomura A., Akiyama M., Itoh H., Yoshino I., Tomomura M., Nishii Y., Noikura T., Sabeki T.;			
RA Coville G.;			
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN [1]			
RP SEQUENCE OF 17-268 FROM N.A.			
RC TISSUE=Pancreas;			
RA Szigoleit A.;			
RA "A human pancreatic chymotrypsin: biochemical and molecular characterization,"			
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Coville G.;			
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.			
RN [3]			
RP SEQUENCE OF 17-268 FROM N.A.			
RC TISSUE=Pancreas;			
RA Szigoleit A.;			
RA "A human pancreatic chymotrypsin gene,"			
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.			
RN [4]			
RP CHARACTERIZATION.			
RX MEDLINE=9820738; PubMed=9538241;			
RA YOSHINO-YASUDA I., KOBAYASHI K., AKIYAMA M., ITOH H., TOMOMURA A., SABEKI T.;			
RA "Caldeocrin is a novel-type serine protease expressed in pancreas, but its homologue elastase IV, is an artifact during cloning derived from caldeocrin gene,"			
J. Biochem. 123:546-554(1998).			
CC -!- FUNCTION: HAS CHYMOTRYPSIN-TYPE PROTEASE ACTIVITY AND HYPOCALCEMIC ACTIVITY.			
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Leu-1-Xaa, Tyr-1-Xaa, Phe-1-Xaa, Met-1-Xaa, Trp-1-Xaa, Gln-1-Xaa, Asn-1-Xaa.			
CC -!- TISSUE SPECIFICITY: PANCREAS.			
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.			
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CC DR EMBL: SB2198; AAB1104_2; ALT_SEQ			
CC DR EMBL: AL031288; CAB7355_1; -.			
CC DR EMBL: Y13697; CAA74031_1; -.			
CC DR HSSP: P00766; 1CHG.			
CC DR MEROPS: S01.157; -.			
CC DR Genew: HGNC:2223; CTRC.			
CC DR Genew: HGNC:2223; CTRC.			



[3] SEQUENCE FROM N.A. (ISOFORM 1).  
 TISSUE=ovary;  
 MEDLINE=99413504; Published=10485494;  
 Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H., O'Brien T.J.; "Cloning of tumor-associated differentially expressed gene-14, a novel serine protease overexpressed by ovarian carcinoma.", Cancer Res. 59:4435-4439(1999).

[4] SEQUENCE FROM N.A. (ISOFORM 1).  
 Gao L., Gellins R., Gown A.M., Moss P., Smith R., Wang K.; "Molecular cloning and characterization of a novel serine protease, ovasin, a potential molecular marker for ovarian carcinomas.", Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

[5] SEQUENCE FROM N.A. (ISOFORM 1).  
 MEDLINE=20510030; Published=11054574;  
 RA Lee I., Lee T., Smith R., Argonza-Barrett R., Lei H., McCuaig J., RA Moss P., Paeser B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.", Gene 257:119-130(2000).

[6] RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).  
 RA Lemerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Diaz J.J., Ramirez M., Stilwagen S., RA Velasco N., Do L., Regala W., Terry A., Brower A., Barnes J., Dangalan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Frankheim M., Attix C., Amico-Keller G., Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronniller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.; "Sequence analysis of chromosome 19q13.4.", Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.

CC -I- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND HIPPOCAMPAL PLASTICITY.  
 CC -I- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPlicing.  
 CC -I- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND PLACENTA. NOT DETECTED IN KIDNEY, SPLEN, LIVER AND LUNG.  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, KALLIKREIN SUBFAMILY.

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CC DR EMBL: AB009849; BAA28673.1; DR SEQUENCE FROM N.A.  
 DR EMBL: AB012761; BAA28676.1; RX MEDLINE=85054882; PubMed=6094548;  
 DR EMBL: AB010780; BAA28684.1; RA Swift G.H., Craig C.S., Stary S.J., Quinto C., Lahate R.G.,  
 DR EMBL: AB008390; BAA28684.1; RA Rutter W.J., Macdonald R.J.;  
 DR EMBL: AB008927; BAA28666.1; RT "Structure of the two related elastase genes expressed in the rat pancreas";  
 DR EMBL: AB055982; ARD56050.1; RL J. Biol. Chem. 259:14271-14278(1984).  
 DR EMBL: AB095742; AAD25979.1; CC -I- FUNCTION ACTS UPON ELASTIN.  
 DR EMBL: AB095743; AAD25974.1; CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Leu-L-Xaa, Met-L-Xaa.  
 DR EMBL: AC243527; ARG33361.1; CC and Phe-L-Xaa. Hydrolyzes elastin.  
 DR HSSP: Q61955; 1NPM. CC -I- SUBCELLULAR LOCATION: Secreted.  
 DR MEROPS: S01.244. CC -I- TISSUE SPECIFICITY: PANCREAS.  
 DR Genew; HGNC:6369; KLKB. CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. ELASTASE SUBFAMILY.  
 DR MM: 603644. CC -----  
 DR InterPro; IPRO01314; Chymotrypsin. CC -----  
 DR InterPro; IPRO01284; Ser\_protease\_Try. CC -----  
 DR Pfam: PF00089; trypsin; 1. CC -----  
 DR PRINTS; PR00722; CHYMOTRYPSIN. CC -----

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SEQUENCE FROM N.A., AND MUTAGENESIS.

RX MEDLINE=21139112; PubMed=11245484;

RA Afar D.E.H.; Vivanco I.; Hubert R.S.; Kuo J.; Chen E.; Saffran D.C.,

RA Rajitano A.B.; Jakobovits A.;

RT "Catalytic cleavage of the androgen-regulated TMPRSS2 protease results in its secretion by prostate and prostate cancer epithelia.";

RL Cancer Res. 61:1686-1692(2001).

[4]

RP TISSUE SPECIFICITY.

RX MEDLINE=2110370; PubMed=11169526;

RA Vaarala M.H.; Porvari K.S.; Kelkumpu S.; Kyllonen A.P.; Viikko P.T.;

RT "Expression of transmembrane serine protease TMPRSS2 in mouse and

RT human tissues.";

FT	DISULFID	172	231	BY SIMILARITY.		RESULT 15
FT	DISULFID	185	241	INTERCHAIN (BY SIMILARITY).		GRAA_HUMAN
FT	DISULFID	244	365	BY SIMILARITY.	ID	GRAA_HUMAN
FT	DISULFID	281	297	BY SIMILARITY.	STANDARD;	STANDARD;
FT	DISULFID	410	426	BY SIMILARITY.	PRT;	PRT;
FT	DISULFID	437	465	BY SIMILARITY.	AC	P12544;
FT	CARBONYD	213	213	N-LINKED (GLCNAC. . .) (POTENTIAL).	DT	01-OCT-1989 (Rel. 12, Created)
FT	CARBONYD	249	249	N-LINKED (GLCNAC. . .) (POTENTIAL).	DT	01-OCT-1989 (Rel. 12, Last sequence update)
FT	VARIANT	449	449	K -> N (IN DBSNP:1056602).	DT	15-JUN-2002 (Rel. 41, Last annotation update)
FT	MUTAGEN	255	255	R->Q: LOSS OF CLEAVAGE.	DE	Granzyme A precursor (EC 3.4.21.78) (Cytotoxic T-lymphocyte proteinase DE 1) (Hanukkina factor) (HF) (Granzyme 1) (CTL tryptase)
FT	MUTAGEN	441	441	S->A: LOSS OF ACTIVITY.	DE	DE 1) (Hanukkina factor) (HF) (Granzyme 1) (CTL tryptase)
FT	CONFFLICT	160	160	M -> V (IN REF. 3).	DE	DE (Fragment 1).
FT	CONFFLICT	242	242	I -> L (IN REF. 1).	DE	GZMA OR CTLA3 OR HFSP.
FT	CONFFLICT	329	329	E -> Q (IN REF. 1).	GN	Hom sapiens (Human).
FT	CONFFLICT	489	491	RAD -> KAN (IN REF. 1).	OS	Cloning and chromosomal assignment of a human cDNA encoding a T
SQ	SEQUENCE	492 AA;	53891 MW;	CAB44FD174A9076B CRC64;	OC	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Query Match		47.8%	Score 66;	DB 1;	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
Best Local Similarity		45.8%	Pred. No. 0.019;	Length 492;	OX	NCBI_TaxID:9606;
Matches		11;	5; Mismatches		OX	NCBI_TaxID:1.
			8;	Indels	RN	[1]
				0;	RP	SEQUENCE FROM N.A.
					RC	TISSUE-Blood;
					RA	Strausberg R.;
					RL	Submitted (Oct'2001) to the EMBL/GenBank/DBJ databases.
					RN	[13]
					RX	TISSUE-T-cell;
					MDLINS:88125000;	PubMed=32557574;
					RA	Gershenson H.K., Herschberger R.J., Shows T.B., Weissman I.L.; Weissman I.L., Shows T.B., Herschberger R.J.,
					RT	"The upstream region of the human granzyme A locus contains both
					RT	"positive and negative transcriptional regulatory elements."
					RL	Submitted (Nov'1995) to the EMBL/GenBank/DBJ databases.
					RN	[14]
					RP	SEQUENCE OF 1-23 FROM N.A.
					RA	Goralski T.J., Krensky A.M.;
					RT	"The upstream region of the human granzyme A locus contains both
					RT	positive and negative transcriptional regulatory elements."
					RL	Submitted (Nov'1995) to the EMBL/GenBank/DBJ databases.
					RN	[15]
					RP	SEQUENCE OF 29-53.
					RA	Poe M., Bennett C.D., Biddison W.E., Blake J.T., Norton G.P.,
					RA	Rodkey J.A., Sigal N.H., Turner R.V., Wu J.K., Zweerink H.J.;
					RT	"Human cytotoxic lymphocyte trypsinase: Its purification from granules
					RT	and the characterization of inhibitor and substrate specificity."
					RL	J. Biol. Chem. 263:13215-13222(1988).
					RN	[15]
					RP	SEQUENCE OF 29-40, AND CHARACTERIZATION.
					RX	MDLINS:89009866; PubMed=226268;
					RA	Hamed A., Lowrey D.M., Lichtenheld M., Podack E.R.;
					RT	"Characterization of three serine esterases isolated from human IL-2 activated killer cells."
					RL	J. Immunol. 141:3142-3147(1988).
					RN	[16]
					RP	SEQUENCE OF 29-39, AND CHARACTERIZATION.
					RX	MDLINS:89035468; PubMed=2263427;
					RA	Krahenbuhl O., Rey C., Jenne D.E., Lanzavecchia A., Grosscurth P.,
					RA	"Characterization of two serine proteinases from cloned human cytotoxic T lymphocytes."
					RA	J. Immunol. 141:3471-3477(1988).
					RN	[17]
					RP	3D-STRUCTURE MODELING.
					RX	MDLINS:89184501; PubMed=3237717;
					RA	Murphy M.E.P., Moult J., Bleackley R.C., Gershenson H., Weissman I.L., James M.N.G.;
					RA	"Comparative molecular model building of two serine proteinases from cytotoxic T lymphocytes."
					RA	Proteins 4:190-204(1988).
					CC	-!- FUNCTION: THIS ENZYME IS NECESSARY FOR TARGET CELL LYSIS IN CELL-MEDIATED IMMUNE RESPONSES. IT CLEAVES AFTER LYS OR ARG. MAY BE INVOLVED IN APOPTOSIS.
					CC	-!- CATALYTIC ACTIVITY: Hydrolysis of proteins, including fibronectin, type IV collagen and nucleolin. Preferential cleavage: Arg- -xaa,
					CC	Lys-1-xaa>>Phe-1-xaa in small molecule substrates.
					CC	-!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.

Qy 1 IVGGXEVTPHAYPWQVGLIFI 20

Db 1 IVGGQEATPHTMVHQVALFI 20

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1, GRANZYME SUBFAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC modified and thus statement is not removed. Usage by and for commercial  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL; M18737; AA52647; 1;  
 DR EMBL; BC015739; AAH15739; 1;  
 DR EMBL; U40006; AAD0009; 1;  
 DR PIR; A28943; A28943.  
 DR PIR; A30525; A30525.  
 DR PIR; A30526; A30526.  
 DR PIR; A31372; A31372.  
 DR PDB; 1HFL; 1HFL; 15-OCT-94.  
 DR MEROPS; S01.135;  
 Genew; HGNC:4708; GZMA.  
 MIM; 140050;  
 DR InterPro; IPR01254; Ser\_protease\_Try.  
 DR Pfam; PF00089; trypsin; 1.  
 DR SMART; SM00020; TRYPSIN\_SPC; 1.  
 DR PROSITE; PS5020; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolyse; Serine protease; Zymogen; Signal; T-cell; Cytolysis;  
 KW Apoptosis; 3D-structure.  
 FT SIGNAL 1 26  
 FT PROPEP 27 28 ACTIVATION PEPTIDE.  
 FT CHAIN 29 262 GRANZYME A.  
 FT ACT\_SITE 69 69 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 114 114 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 54 70 BY SIMILARITY.  
 FT DISULFID 148 218 BY SIMILARITY.  
 FT DISULFID 179 197 BY SIMILARITY.  
 FT DISULFID 208 234 BY SIMILARITY.  
 FT CARBOHD 170 170 N-LINKED (GLUCNAC, ... ) (POTENTIAL).  
 SQ SEQUENCE 262 AA; 28968 MW; DA87563A0B92BAF4 CR064;

Query Match 47.1%; Score 65; DB 1; Length 262;  
 Best Local Similarity 57.1%; Pred. No. 0.014;  
 Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

1 IVGGXETPHAYPWQVGFID 21  
 1:1:1:1:1:1:1:1:1:  
 29 IIGGNEVTPHSRPMVLLSLD 49

Search completed: May 30, 2003, 11:02:43  
 Job time : 23 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 10:57:47 ; Search time 79 Seconds  
(without alignments)

65.205 Million cell updates/sec

Title: US-09-549-642-20

Perfect score: 138

Sequence: 1 IVGCGXEVTPHAYPKVQGLFIDDMYF 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

1 number of hits satisfying chosen parameters:

671580

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rabbit:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriopl:\*
- 17: sp\_archeapl:\*

## ALIGNMENTS

RESULT 1					
ID	AC	DT	DT	DE	GN
O18487	O18487/	01-JAN-1998	(TREMBLrel. 05, Created)		
		01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
			Chymotrypsin BI (Fragment).		
				Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;	
					OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
					OC Penaeidae; Litopenaeidae; NCBI_TaxID=6689;
					RN (1)
					RP SPOUSE FROM N_A,
					RC TISSUE-SPERMATOPHORUS;
					RX MEDLINE-99331490; Published-10407165;
					RT "Polymorphism and evolution of collagenolytic serine protease genes in
					RT crustaceans."
					RL Blochim. Biophys. Acta 1432:419-424(1999).
					CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
					CC EMBL TRYPsin FAMILY.
					DR PRINTS: PFO089; trypsin; 1.
					DR HSSP: P00771; IAVZ.
					DR MEROPS: S01-122; -.
					DR InterPro: IPR001314; Chymotrypsin.
					DR InterPro: IPR001254; Ser_protease_Try.
					DR PFM: PF0089; trypsin; 1.
					DR PRINTS: PRO0022; CHYNOTRYPSIN.
					DR SMART: SM00020; Tryp_SPC; 1.
					DR PROSITE: PS001240; TRYPSIN_HIS; UNKNOWN_1.
					DR PROSITE: PS00134; TRYPSIN_SER; 1.
					DR Hydrolase; Serine protease.
					ET NON_TER 271
					SQ SEQUENCE 271 AA; 28743 MW; EAD3F41DD6053ADE CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	101	73.2	271	5	O18487	018487 penaeus van
2	95	68.8	270	5	O8wrl1	O8wrl1 parathiole
3	94	68.1	265	5	O18488	O18488 penaeus van
4	89	64.5	270	5	O27824	O27824 uca pugilat
5	77	55.8	254	6	O9xsn6	O9xsn6 sus scrofa
6	76	55.1	474	5	Q8t4n3	Q8t4n3 hippocampal
7	74	53.6	309	5	O27083	O27083 tachypodus
8	72	52.2	255	11	O9z0m1	O9z0m1 mus musculus
9	72	52.2	255	11	Q930m1	Q930m1 mus musculus
10	72	52.2	270	5	O96871	O96871 trichinella
11	71	51.4	465	5	O9BBL7	O9BBL7 trichinella
12	69	50.0	467	5	Q967X8	Q967X8 panulirus a
13	69	50.0	868	5	O9TIV3	O9TIV3 polyandros
14	69	50.0	1524	13	O91674	O91674 xenopus lae
15	67	48.6	263	13	Q9PWQ6	Q9PWQ6 gadus morhua
16	66	47.8	260	13	Q9w7q3	Q9w7q3 paralichthys

Query Match	73.2%	Score 101; DB 5; Length 271;	CC TRYPSIN FAMILY
Best Local Similarity	72.0%	Pred. No. 3.6e-5;	DR EMBL: Y10665; CAA71673.1; -.
Matches 18;	Conservative	2; Mismatches 5;	DR HSSP: P00771; JAZZ.
Matches 18;	Created)	Indels 0;	DR MEROPS: S01.122; -.
Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25	DR Interpro: IPR001314; Chymotrypsin.	Gaps 0;	DR Interpro: IPR001254; Ser_protease_Try.
Db 46 IVGGVEATPHSMWPHQALFIDDMYF 70	PFam: PF00089; trypsin; 1.		DR PFam; PRO0722; CHYMOTRYPSIN.
RESULT 2	SMART: SM00020; TRYD_SPC; 1.		DR SMART: SM00020; TRYD_SPC; 1.
Q8WR11 ID Q8WR11; PRELIMINARY; PRT; 270 AA.	DR PROSITE; PS50240; TRIPSIN_DOM; 1.		DR PROSITE; PS50240; TRIPSIN_DOM; 1.
AC 08WR11; (TREMBLrel. 20; Created)	DR PROSITE; PS00134; TRIPSIN_HIS; UNKNOWN_1.		DR PROSITE; PS00135; TRIPSIN_SER; 1.
DT 01-MAR-2002 (TREMBLrel. 20; Last sequence update)	KW Hydrolase; Serine protease; Signal.		DR PROSITE; PS00135; TRIPSIN_SER; 1.
DT 01-JUN-2002 (TREMBLrel. 21; Last annotation update)	FT NON_TER 1		FT NON_TER 1
DE Collagenolytic serine protease.	FT SIGNAL <1		FT SIGNAL <1
OS Paralithodes camtschatica (Kamchatka crab) (Red king crab).	FT NON_TER 265		FT NON_TER 265
C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea; Lithodidae; Paralithodes.	SEQUENCE 265 AA; 27895 MW; E6F6FC216C2ECB63 CRC64;		SEQUENCE 265 AA; 27895 MW; E6F6FC216C2ECB63 CRC64;
[1]	Query Match Score 94; DB 5; Length 265;		Query Match Score 94; DB 5; Length 265;
RN RP SEQUENCE FROM N.A. Kisiltsitsin Y.A., Rebkirkov, D.V., Kuranova I.P.: RA Rudenskaya G.N., Kisiltsitsin Y.A., Rebkirkov, D.V., Kuranova I.P.: RT "King crab Paralithodes camtschaticus Collagenolytic serine protease PC King crab cloning, primary structure and molecular RT PC and Trypsin PC: cDNA cloning, primary structure and molecular RT modeling of the enzymes".	Best Local Similarity 68.0%; Pred. No. 4e-06;		Best Local Similarity 68.0%; Pred. No. 4e-06;
RT J. Protein Chem. 0:0-0(2002).	Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;		Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
RL DR EMBL: AF461035; AAL67441.1; -.	RESULT 4		RESULT 4
DR Interpro: IPR001314; Chymotrypsin.	Q27824 ID Q27824 PRELIMINARY; PRT; 270 AA.		Q27824 ID Q27824 PRELIMINARY; PRT; 270 AA.
DR Interpro: IPR001254; Ser_protease_Try.	AC Q27824; 01-NOV-1996 (TREMBLrel. 01; Created)		AC Q27824; 01-NOV-1996 (TREMBLrel. 01; Created)
DR PFam: PF00089; trypsin; 1.	DT 01-NOV-1996 (TREMBLrel. 01; Last sequence update)		DT 01-NOV-1996 (TREMBLrel. 21; Last annotation update)
DR PRINTS: PRO0722; CHYMOTRYPSIN.	DR Serine collagenase 1 precursor (EC 3.4.21.32).		DR Serine collagenase 1 precursor (EC 3.4.21.32).
DR SMART: SM00020; TRYD_SPC; 1.	DR Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).		DR Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
DR PROSITE; PS50240; TRIPSIN_DOM; 1.	DR OC Metuzoia: Metuzoia; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Subbrachyura; Ocyopodaidea; Ocyopoda; Ocyopodinae; Uca complex; Celuca.		DR OC Metuzoia: Metuzoia; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Subbrachyura; Ocyopodaidea; Ocyopoda; Ocyopodinae; Uca complex; Celuca.
DR PROSITE; PS00134; TRIPSIN_HIS; UNKNOWN_1.	OX NCBI_TaxID=6772;		OX NCBI_TaxID=6772;
DR PROSITE; PS00135; TRIPSIN_SER; UNKNOWN_1.	RN [1] SEQUENCE FROM N.A.		RN [1] SEQUENCE FROM N.A.
KW Protease.	RP TISSUE=HEPATOPANCREAS;		RP TISSUE=HEPATOPANCREAS;
SQ SEQUENCE 270 AA; 28157 MW; 0CDIF574C5C1BD52 CRC64;	RC MEDLINE=9612234; PubMed=8626718;		RC MEDLINE=9612234; PubMed=8626718;
Query Match 68.8%; Score 95; DB 5; Length 270;	RA TSU.C.A.; Craik C.S.;		RA TSU.C.A.; Craik C.S.;
Best Local Similarity 72.0%; Pred. No. 2.9e-06;	RT "Substrate" recognition by recombinant serine collagenase 1 from Uca		RT "Substrate" recognition by recombinant serine collagenase 1 from Uca
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE CC TRYPSIN FAMILY		-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE CC TRYPSIN FAMILY
Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25	DR DR		DR DR
Db 45 IVGGVEATPHTWVHQVALFIDDMYF 69	DR MEROPS: S01.122; -.		DR MEROPS: S01.122; -.
RESULT 3	DR Interpro: IPR001314; Chymotrypsin.		DR Interpro: IPR001314; Chymotrypsin.
O18488 ID O18488; PRELIMINARY; PRT; 265 AA.	DR PFam: PF00089; trypsin; 1.		DR PFam: PF00089; trypsin; 1.
AC 018488; (TREMBLrel. 05; Created)	DR PRINTS: PRO0722; CHYMOTRYPSIN.		DR PRINTS: PRO0722; CHYMOTRYPSIN.
DT 01-JAN-1998 (TREMBLrel. 05; Last sequence update)	DR PROSITE; PS50240; TRIPSIN_DOM; 1.		DR PROSITE; PS50240; TRIPSIN_DOM; 1.
DT 01-JUN-2002 (TREMBLrel. 21; Last annotation update)	DR PROSITE; PS00134; TRIPSIN_HIS; UNKNOWN_1.		DR PROSITE; PS00134; TRIPSIN_HIS; UNKNOWN_1.
DB CHYMOTRYPSIN B.	KW Collagen; Hydrolase; Serine protease; Signal.		KW Collagen; Hydrolase; Serine protease; Signal.
GN Penaeus vannamei (Penaeid shrimp) (European white shrimp).	FT SIGNAL 15		FT SIGNAL 15
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Penaeoidea; Penaeidae; Litopenaeus.	FT CHAIN 45		FT CHAIN 45
OC Penaeidae; Litopenaeus.	SEQUENCE 270 AA; 28170 MW; C0BAD974568ED887 CRC64;		SEQUENCE 270 AA; 28170 MW; C0BAD974568ED887 CRC64;
RN [1] SEQUENCE FROM N.A.	Query Match Score 89; DB 5; Length 270;		Query Match Score 89; DB 5; Length 270;
RC TISSUE=SPERMATOPHORUS; MEDLINE=93337450; PubMed=10407165;	Best Local Similarity 64.0%; Pred. No. 2.3e-05;		Best Local Similarity 64.0%; Pred. No. 2.3e-05;
RA Sellous D.Y.; Van Wormhoudt A.;	Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;		Matches 16; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
RT "Polymorphisms and evolution of collagenolytic serine protease genes in crustaceans.";	Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25		Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25
RT Biochim. Biophys. Acta 1432:419-424 (1999);	Db 45 IVGGVEATPHTWVHQVALFIDDMYF 69		Db 45 IVGGVEATPHTWVHQVALFIDDMYF 69
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE			



of mouse cDNA.";  
 [2] RT J. Dent. Res. 79:70-76(2000).  
 RN  
 RP SEQUENCE FROM N A.  
 STRAIN-SWISS-WEBSTER;  
 MEDLINE=20323211; PubMed=10863090;  
 RX Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;  
 RA "Characterization of the mouse and human PRSS17 genes, their  
 relationship to other serine proteases, and the expression of PRSS17  
 in developing mouse incisors";  
 RR Gene 25:1-8(2000).  
 :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPsin FAMILY.  
 DR EMBL: AF198031; AAC88944.; -.  
 HSSP: P00763.; IDPO.  
 DR MEROPS: S01\_251.; -.  
 DR MGI: MGI:1861379; KlK4.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 PRINTS: PRO00722; CHYMOTRYPSIN.  
 SMART: SM00020; Tryp\_SPC; 1.  
 DR PROSITE: PS550240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease; Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 SQ CHAIN 32 255 MATRIX SERINE PROTEINASE 1.  
 SEQUENCE 255 AA; 27488 MW; 6FD2E7DEA0660A2A CRC64;

Query Match 52.2%; Score 72; DB 11; Length 255;  
 Best Local Similarity 44.0%; Pred. No. 0.0076; Indels 0; Gaps 0;  
 Matches 11; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLFIDDMYF 25  
 Db 32 IIQGQDCSPHSQWQAALFSEDFGF 56

RESULT 10  
 096871 PRELIMINARY; PRT;  
 ID 096871 IDPO.  
 AC 096871\_01-MAY-1999 (TRMBLrel. 10, Created)  
 DT 01-MAY-1999 (TRMBLrel. 10, Last sequence update)  
 DR 01-MAR-2002 (TRMBLrel. 20, Last annotation update)  
 DE Serine proteinases.  
 OS Trichinella spiralis.  
 OC Eukaryota; Metazoa; Nemataoda; Enopilea; Trichocephalida;  
 OC Trichinellidae; Trichinella.  
 NCBI\_TaxID=6334; [1]

RN [1]  
 RP SEQUENCE FROM N A.  
 RA Todorova V., Xia Y., Moore J., Kennedy M.W.;  
 RT "A cDNA encoding a stage-specific serine proteinase of Trichinella  
 spiralis."  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.  
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPsin FAMILY.  
 DR EMBL: U62653; AAC09211.1; -.  
 DR HSSP: P00733; IDPO.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR PRINTS: PRO00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; Tryp\_SPC; 1.  
 DR PROSITE: PS550240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease.  
 SQ SEQUENCE 270 AA; 6E5233084FBB13B7 CRC64;  
 DR HSSP: P00733; IDPO.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR PRINTS: PRO00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; Tryp\_SPC; 1.  
 DR PROSITE: PS550240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase; Serine protease.  
 SQ SEQUENCE 270 AA; 6E5233084FBB13B7 CRC64;

Query Match 52.2%; Score 72; DB 5; Length 270;  
 Best Local Similarity 60.0%; Pred. No. 0.008; Indels 6; Mismatches 2; Gaps 0;

Qy 1 IVGGXEVTPHAYPWQVGLF1 20  
 Db 39 IVGGSDAVPHSYSPWQAHLSI 58

RESULT 11  
 Q9BJL7 PRELIMINARY; PRT;  
 ID Q9BJL7 IDPO.  
 AC Q9BJL7\_01-JUN-2001 (TRMBLrel. 17, Created)  
 DT 01-JUN-2001 (TRMBLrel. 17, Last sequence update)  
 DR 01-JUN-2002 (TRMBLrel. 21, Last annotation update)  
 DE Newborn larva-specific serine protease SS2.  
 OS Trichinella spiralis.  
 OC Eukaryota; Metazoa; Nemataoda; Enopilea; Trichocephalida;  
 OC Trichinellidae; Trichinella.  
 NCBI\_TaxID=6334; [1]

RN [1]  
 RP SEQUENCE FROM N A.  
 STRAIN-129-SVJ;  
 MEDLINE=2023211; PubMed=10863090;  
 RX Hu J.C., Zhang C., Sun X., Yang Y., Cao X., Ryu O., Simmer J.P.;  
 RA "Characterization of the mouse and human PRSS17 genes, their  
 relationship to other serine proteases, and the expression of PRSS17  
 in developing mouse incisors";  
 RR Gene 25:1-8(2000).  
 :- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPsin FAMILY.  
 DR EMBL: AF198031; AAC88937.1; -.  
 DR HSSP: P00763.; IDPO.  
 DR MEROPS: S01\_251.; -.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR PRINTS: PRO00722; CHYMOTRYPSIN.  
 SMART: SM00020; Tryp\_SPC; 1.  
 DR PROSITE: PS550240; TRYPSIN\_DOM; 1.

RESULT	ID	SEQUENCE	PRT	AA
12	Q967X8	PRELIMINARY;		467 AA.
	AC	Q967X8;		
	DT	01-DEC-2001 (TREMBLrel. 19, Created)		
	DT	01-JUN-2002 (TREMBLrel. 19, Last sequence update)		
	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
	DE	CUB-serine protease.		
	OS	Panulirus argus (Spiny lobster).		
	OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Euvelida; Decapoda; Pleocyemata; Palinura; Palinuroidea; Palinuridae; Panulirus.		
	OX	NCBI_TaxID=6737;		
	RN	[1]		
	RP	SEQUENCE FROM N.A.		
	RA	Levine M.J., Walthall W.W., Tai P.C., Derby C.D.; Molecular cloning, characterization, cellular localization and possible function of a CUB-serine protease in the olfactory system of the spiny lobster Panulirus argus.		
	RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
	EMBL:	AF357226; AAC48894; -		
	DR	IPR000855; CUB_domain.		
	DR	InterPro; IPR001251; Ser_protease_TRY.		
	DR	Pfam: PF00431; CUB; 1.		
	DR	Pfam; PF00089; Trypsin; 1.		
	DR	PROSITE; PS01180; CUB; 1.		
	DR	PROSITE; PS50240; TRYPSIN_DOMAIN; 1.		
	DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.		
	DR	PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.		
	KW	Hydrolase; Protease; Serine protease.		
	SEQUENCE	467 AA; 50453 MW;		
	SQ	1D2E563D314BBFD CRC64;		
	Query Match	50.0%	Score 69; DB 5;	Length 467;
	Best Local Similarity	58.3%	Fed. No. 0.039;	
	Matches 14;	Conservative	Mismatches 1;	Gaps
			Indels 9;	
	Qy	1 IVGGXEVTPHAYPWQVGLFIDDMY 24		
	Db	229 IVGGQETEVNEYWPQWQLVLYTRDMY 252		

RESULT 13												
Q9Y1V3		PRELIMINARY;		PRT; 868 AA.								
ID	Q9Y1V3											
AC	Q9Y1V3;											
DT	01-NOV-1999	(TREMBLrel.	12.	Created)								
DT	01-NOV-1999	(TREMBLrel.	12.	Last sequence update)								
DT	01-JUN-2002	(TREMBLrel.	21.	Last annotation update)								
DE	Tunicate retinoidic acid-inducible modular protease precursor.											
GN	TRAMP.											
OS	Polypandrocarpa misakiensis.											
OC	Eukaryota; Metazoa; Chordata; Ascidiacea;											
OC	Stolidobranchia; Styelidae; Polyandrocarpa.											
NCBI-TaxID	7722;											
RN	[1]											
RP	SEQUENCE FROM N.A.											
RC	STRAIN=WHITE SPOT;											
RX	MEDLINE=9923666; PubMed=10491255;											
RA	Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;											
RT	A retinoic acid-inducible modular protease in budding ascidians.											
RL	Dev. Biol. 214: 38-45 (1998).											
CC	-1 SIMILARITY. BELONGS TO PEPTIDASE FAMILY 51; ALSO KNOWN AS THE TRYPSIN FAMILY.											
CC	EMBL: AB030007; BAA82522; 1 - .											
DR	HSSP: P00763; IDPO.											
DR	InterPro: IPR01314; Chymotrypsin.											
DR	InterPro: IPR002172; LDL_recept_A.											
DR	InterPro: IPR003609; Pan_app.											
DR	InterPro: IPR01254; Ser_protease_tryp.											
DR	InterPro: IPR001190; Sscr_receptor.											
DR	PFam: PF00057; ldl_recept_A; 3.											
DR	PFam: PF00530; SRCR; 2.											
DR	PFam: PF00089; trypsin; 1.											
DR	PRINTS: PR00722; CHYMOTRIPSIN.											
DR	PRINTS: PR02614; LDRECEPTOR.											
DR	PRINTS: PS00258; SPERACTRCPTR.											
DR	SMART: SM00192; LDLA; 3.											
DR	SMART: SM00473; PAN_AP; 1.											
DR	SMART: SM00202; SR; 2.											
DR	SMART: SM00020; TRYP_SPC; 1.											
DR	PROSITE: PS01209; LDLRA_-; 3.											
DR	PROSTE: PS50098; LDLRA_-; 3.											
DR	PROSTE: PS50027; SPGR2; 2.											
DR	PROSTE: PS50210; TRYSIN_DOM; 1.											
DR	PROSTE: PS00134; TRYSIN_HIS; UNKNOWN_1.											
DR	PROSTE: PS00135; TRYSIN_SER; 1.											
KW	Glycoprotein; Hydrolase; Protease; Serine protease; Signal.											
FT	SIGNAL 1 28 POTENTIAL_AA:											
SQ	SEQUENCE 868 AA; 97660 MW; F71462865F36f6CA CRC64;											
Query Match 50.0% Score 69; DB 5; Length 868;												
Best Local Similarity 44.0% pred. No. 0.074; Matches 5; Mismatches 9; Indels 0; G												
Qy	1 IVGGXETPHAPWQVGLLFDDMVF 25											
Db	624 IVGGSSTEPHFWPQAGIWLPTWY 648											

  

RESULT 14						
Q91674		PRELIMINARY;		PRT; 1524 AA.		
ID	Q91674					
AC	Q91674;					
DT	01-NOV-1996	(TREMBLrel.	01.	Created)		
DT	01-NOV-1998	(TREMBLrel.	08.	Last sequence update)		
DT	01-JUN-2002	(TREMBLrel.	21.	Last annotation update)		
DE	Polyprotein.					
OS	Xenopus laevis (African clawed frog).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Anura; Batrachia; Anura; Mesobatrachia; Pipidae;					
OC	Xenopodinae; Xenophidae; Stolidobranchia; Styelidae; Polyandrocarpa.					
NCBI-TaxID	8355;					
RN	SEQUENCE FROM N.A.					
RP	SEQUENCE FROM N.A.					

RX MEDLINE=99432219; PubMed=10500163;  
 RA Lindsay L.L., Yang J.C., Hedrick J.L.;  
 "Ovochymase, a Xenopus laevis egg extracellular protease, is  
 translated as part of an unusual polypeptide",  
 Proc. Natl. Acad. Sci. U.S.A. 96:11253-11258(1999).  
 [2]  
 RN  
 RP SEQUENCE FROM N.A.  
 RA Yang J.C., Lindsay L.L., Hedrick J.L.;  
 "cDNA Cloning of Ovochymase, a Chymotrypsin-like Protease Released  
 From Xenopus laevis Eggs at Fertilization.",  
 Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: CONTAINS 4 CUB DOMAINS.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPsin FAMILY.  
 EMBL: UB1290; AAC24717.1; -  
 DR HSSP; P00763; 1DPO.  
 DR MEROPS; S01.022; -  
 DR MEROPS; S01.245; -  
 InterPro; IPR001314; Chymotrypsin.  
 InterPro; IPR000859; CUB\_domain.  
 InterPro; IPR001254; Ser\_protease\_Try.  
 Pfam; PF00431; CUB; 5.  
 Pfam; PF00089; Trypsin; 3.  
 DR PRINTS; PR00722; CHYMTROPSIN.  
 SMART; SM00042; CUB; 4.  
 SMART; SM00020; TRYPSIN\_SPC; 3.  
 PROSITE; PS01180; CUB; 5.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 3.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_3.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 3.  
 KW Hydrolase; Serine protease.  
 FT CHAIN 57 308 SERINE PROTEASE.  
 FT CHAIN 584 817 SERINE PROTEASE.  
 FT CHAIN 1295 1524 OVOCHYMASE.  
 SQ SEQUENCE 1524 AA; 167566 MW; 32EFE42128F37268 CRC64;  
 DR  
 Query Match Score 69; DB 13; Length 1524;  
 Best Local Similarity 57.9%; Pred. No. 0.13;  
 Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 IVGGXEVTPHAYPWQVGLF 19  
 |||| | : : : : : : : : : :  
 Db 584 IVGGEAASPNSWPWQVIF 602

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RESULT 15  
 OPIPH06 PRELIMINARY; PRT; 263 AA.  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PYLORIC CAECAL;  
 RX MEDLINE=2046434; PubMed=11011764;  
 RA Spiliard R., Guadmundsdottir A.;  
 RT "Molecular Cloning of the Atlantic Cod Chymotrypsinogen B";  
 RL Microb. Comp. Genomics 5:41-50(2000).  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE  
 TRYPsin FAMILY.  
 EMBL: AD42521; CAB43766.1; -  
 DR HSSP; P00766; ICIG.  
 DR MEROPS; S01.157; -  
 InterPro; IPR001314; Chymotrypsin.  
 InterPro; IPR001254; Ser\_protease\_Try.